

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2005, 16:44:00 ; Search time 4555 Seconds
(without alignments)
10956.942 Million cell updates/sec

Title: US-10-089-278-1
Perfect score: 1030
Sequence: 1 tccaccactctgactcaag.....ccagccagtcagttttatc 1030

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1030	100.0	1030	6	AX111694 Sequence
2	644	62.5	990	6	AX111696 Sequence
3	629.2	61.1	946	6	AX111697 Sequence
4	598.8	58.1	927	6	AX111695 Sequence
5	564.6	54.8	1632	12	SYN507107
6	544.4	52.9	1695	12	SC0544530
7	542.4	52.7	744	12	AF402256
8	538	52.2	2190	6	AX100186
9	537.6	52.2	876	6	AX100194
10	537.4	52.2	969	6	AX100188
11	524	50.9	795	10	MMSCFVP25
12	522.6	50.7	925	6	E30617
13	508.4	49.4	687	12	AF003707
14	505	49.0	1817	6	AX739887
15	497.6	48.3	882	12	SC0278109
16	496.2	48.2	687	12	AF003705
17	487.6	47.3	897	6	CQ881538
18	486	47.2	1314	6	A68604
19	483	46.9	993	6	AX798477

20	482.2	46.8	1698	6	BD206134	Polyvalen
21	482.2	46.8	1698	6	AX011206	Sequence
22	481.4	46.7	888	6	AX100192	Sequence
23	480.2	46.6	2199	6	AX100182	Sequence
24	479.2	46.5	978	6	AX100184	Sequence
25	478.6	46.5	717	6	AR482235	Sequence
26	474.2	46.0	4354	12	ASY14583	Artificial
27	471	45.7	732	12	AY725472	Synthetic
28	467	45.3	747	12	AF226875	Synthetic
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30	460.4	44.7	1906	6	AX777477	Sequence
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32	457	44.4	1653	6	BD206135	Polyvalen
33	457	44.4	1653	6	AX011208	Sequence
34	455.4	44.2	739	6	A97141	Sequence
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39	447.8	43.5	747	6	AX100178	Sequence
40	447	43.4	1817	6	AX739885	Sequence
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43	440.8	42.8	753	12	SC0416563	Synthetic
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ALIGNMENTS

RESULT 1
AX111694
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

AX111694
Sequence 1 from Patent WO0125415.
AX111694
AX111694.1 GI:13927959
synthetic construct
synthetic construct
other sequences; artificial sequences.
1
Cichutek, K. and Engelstaedter, M.
Gene transfer in human lymphocytes using retroviral scfv cell targeting
Patent: WO 0125415-A 1 12-APR-2001;
Bundesrepublik Deutschland LET (DE)
Location/Qualifiers
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/note="scFv kodierende Sequenz"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.9e-269;
Matches 1030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 TCCACCACCTCTCGACTCAAGAAAGCTCTGACACCAAGAAAGTGTCTGTCTCCACCA 60
QY 61 CTCCGATCCGCTGAGGGTAAAGTTGACCGAGCGAGCAAAATCCTAATTCCTCTGTGGC 120
DB 61 CTCCGATCCGCTGAGGGTAAAGTTGACCGAGCGAGCAAAATCCTAATTCCTCTGTGGC 120
QY 121 TTGGTGGGGGTTGGGACCACTGCCGAAAGTTTCAGCTGCCGAGCGGCCGCGCCAT 180
DB 121 TTGGTGGGGGTTGGGACCACTGCCGAAAGTTTCAGCTGCCGAGCGGCCGCGCCAT 180
QY 181 GGCCGAGGTCAGCTGCACAGCTCAGGGGCTGAGCTGGTGGCCCTCAGTGA 240


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QY 944 GGCTCCGGGGCGGTGGTTC---TGTGGTGGTTCGTGGTGGTGGTGGTGGT 1000
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QY 1001 GGTTCGGGCCAGCCAGTCCAGTTTATC 1030
Db 934 GGTTCGGGCCAGCCAGTCCAGTTTATC 963

RESULT 3
AX111697
LOCUS AX111697 946 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 4 from Patent WO0125415.
ACCESSION AX111697
VERSION AX111697.1 GI:13927962
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Cichutek, K. and Engelstaedter, M.
TITLE Gene transfer in human lymphocytes using retroviral scfv cell
JOURNAL targeting
Patent: WO 0125415-A 4 12-APR-2001;
Bundesrepublik Deutschland LET (DE)
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Query Match 61.1%; Score 629.2; DB 6; Length 946;
Best Local Similarity 80.2%; Pred. No. 3.4e-160;
Matches 768; Conservative 0; Mismatches 178; Indels 12; Gaps 2;

QY 44 ATGGACTGTCTACCAACCTCCGATCCGCTGAGGGTAAAGTTGACAGCGGAGCAAAATC 103
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QY 104 CTAATTTCTCTTGTGGCTTGTGGGGTTTGGGACCACTGCCAGCTTCGACTGCCCGA 163
Db 61 CTAATTTCTCTTGTGGCTTGTGGGGTTTGGGACCACTGCCAGCTTCGACTGCCCGA 120
QY 164 GCGGCCAGCCGCGCCATGCGCGAGGTCAAGCTGCAGAGTCAGGGGCTGAGCTGTGAGG 223
Db 121 GCGGCCAGCCGCGCCATGCGCGAGGTCAAGCTGCAGAGTCAGGGGCTGAGCTGTGAGG 180
QY 224 CTTGGGGTCTCAGTGAAGATTTCTGCGAAGGGTTCTGGCTACACATCTCAGTTATGGT 283
Db 181 CTTGGAGCTTCAAGTGAAGCTGTCTGCAAGACTTCTGGCTTCTCCTTACCAGCTACTGG 240
QY 284 ATGAGCTGGGTGAAACAGAGTCAATGCAAGAGTCTAGAGTGGATTCGACTTATTAGTACT 343
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QY 404 AAATCTCCACACAGCCCTATTGGAACTTTGGAACTTGGCAGACTGACATCTGAGGATTCGCAAT 463
Db 361 AAATCTCCACACAGCCCTACATGCAACTCAGCAGCCCGACATCTGAGGACTCTGCGGTC 420
QY 464 TATTATTGGCAAGATCCGATGTTATACGGGTATTATGCTTTGACTTGGACTTGGGC 523
Db 421 TATTACTGCAAGATCTCTTTATGCTAAC---TACCCCTCTCTGGTTTACTTACTGGGCG 477
QY 524 CAAGGCACTACCGTCTACCGTCTCTCAGGTGGAGGGGTTTACGGCGAGGTGGCTCTGGC 583
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QY 584 GGTGGCGGATCGGATATCGAGTCACTCAGTCTCCATCTTCTTTGGCTGTGTCTCTAGGG 643
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QY 644 CAGAGGGCCACCATATCTCTGCAGAGCAGTGAAGAGTGTGATAGTTATGGCGATAGTTT 703
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QY 704 ATGCACTGTATCAGCAGAAACAGACAGCCACCAAACTCCTCATCTATCTATCGTCATCC 763
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QY 764 AACCTAGAATCTGGAGTCCCTGCCAGTTTCAGTGGCAGTGGGCTCAGTCAGTCAGACTTCACT 823
Db 709 AATCTGGCTTCTGGAGTCCAGCTCCGCTTCAGTGGCAGTGGGCTCTGGACCTCTTACTCT 768
QY 824 CTCACCATCGATCTCTGTGGAGGAAGATGATGCTGCAGTGTATTACTGTCTGCAAGTATG 883
Db 769 CTCACAATTGGCACCATGGAGGCTGAAGATGTTGCCACTTACTTCCAGCAGGGTAGT 828
QY 884 GAAGATCCCTACAGTTTCGAGGGGGACCAAGCTGGAATAAAACGGCGCGCGCATCG 943
Db 829 AGTATACCTTACACAGTTTCGAGGGGGACCAAGCTGGAATAAAACGGCGCGCGCATCG 888
QY 944 GGCTCCGGGGCGGTGGTTCGTGGTGGTTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1001
Db 889 GGCTCCGGGGCGGTGGTTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 946

RESULT 4
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LOCUS AX111695 927 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 2 from Patent WO0125415.
ACCESSION AX111695
VERSION AX111695.1 GI:13927960
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Cichutek, K. and Engelstaedter, M.
TITLE Gene transfer in human lymphocytes using retroviral scfv cell
JOURNAL targeting
Patent: WO 0125415-A 2 12-APR-2001;
Bundesrepublik Deutschland LET (DE)
FEATURES
source
1. .927
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ORIGIN
Query Match 58.1%; Score 598.8; DB 6; Length 927;
Best Local Similarity 78.6%; Pred. No. 6.5e-152;
Matches 755; Conservative 0; Mismatches 172; Indels 33; Gaps 2;

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QY 44 ATGGACTGTCTCACCACCTCCGATCCGCTGAGGGTAAAGTTGACAGCGGAGCAAAATC 103
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QY 104 CTAATTTCTCTTGTGGCTTGTGGGGTTTGGGACCACTGCCGAAAGTTTCGACTGCCCGA 163
Db 61 CTAATTTCTCTTGTGGCTTGTGGGGTTTGGGACCACTGCCGAAAGTTTCGACTGCCCGA 120
QY 164 GCGGCCAGCCGCGCCATGCGCGAGTCAAGCTGCAGAGTCAAGGGCTCAGCTGGTGAGG 223
Db 121 GCGGCCAGCCGCGCCATGCGCGAGTCAAGCTGCAGAGTCAAGGGCTCAGCTGGTGAGG 180
QY 224 CTTGGGGTCTCAGTGAAGATTTCTGCAAGGGTCTTGGCTACACATTCATGATTATGCT 283
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Best Local Similarity 85.2%; Pred No. 1.4e-142;	
Matches 643; Conservative 0; Mismatches 109; Indels 3; Gaps 1;	
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Qy 246	CCTGCAAGGGTTCGGCTACACATTCATCATGATTATGCTGAGCTGGGTGAAACAGAGTC 305
Db 917	CCTGCAAGCTTCCTGGCTACCGATTCAGTAGGTGTGGATGAACCTGGGTGAAGCAGAGC 976


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Qy 306 ATGCAAGAGCTAGAGTGGAGTCTATTAGTACTTACTATGGTGACTCTAGTTTACA 365
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Qy 426 TGGAACTGCGACACTGACATCTGAGGATTCGCGATTTATTATTATGTGCAAGATCGGATG 485
Db 1097 TGCAGGTCAGCAGCCTGACCTCTGTGGACTCTGCGGTCTATTCTGTGCAAGAGGGAA-- 1154
Qy 486 GTAATTACGGGTATTACTATGCTTTTGGACTACTGGGCGCAAGGCACTACCGTCAACGCTCT 545
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Qy 546 CCTCAGGTGAGGCGGTTTCAAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAGC 605
Db 1214 CCTCAGGTGAGGCGGTTTCAAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGATCGAGC 1273
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Db 1274 TCACTAGTCTCCAGTCTTCTTTGGCTGTGTCTCTAGGGCAGAGGCCACCATATCTCTGCA 1333
Qy 666 GAGCAGTGAAGTGTGTAGTATTGCGGATAGTTTATTATGCACTGGTATCAGCAGAAC 725
Db 1334 GAGCAGTGAAGTGTGTAGTATTGCGGATAGTTTATTATGCACTGGTATCAGCAGAAC 1393
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Db 1394 CAGGACAGCCCAAACTCTCATCTATCTTGCATCCAACTAGAACTCTGGAGTCCCTG 1453
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Qy 906 GGGGACCAAGCTGGAATAAAACGGGCGGCCGCA 940
Db 1574 GGGGACCAAGCTGGAAGTCAAAACGGGCGGCCGCA 1608

RESULT 6
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LOCUS
DEFINITION
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  clone r95M.
ACCESSION
  AJ544530
VERSION
  AJ544530.1 GI:28804184
KEYWORDS
  antibody; heavy chain; immunoglobulin; light chain; scFv; variable
  region.
SOURCE
  synthetic construct
  ORGANISM
    other sequences; artificial sequences.
  1 (bases 1 to 1695)
  Grosse-Hovest,L.
  Direct Submission
  Submitted (14-FEB-2003) Grosse-Hovest L., Immunology, University of
  Tuebingen, Auf der Morgenstelle 15, 72076 Tuebingen, GERMANY
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Db 920 CCTGCAAGGTTCTGGCTACACATTCAGTAGGTCTTGGATGAACACAGAGGC 979
Qy 306 ATGCAAGAGTCTAGAGTGGATTTAGTACTTATTAGTACTTACTAGTCTCTAGTTTACA 365
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  Best Local Similarity 83.6%; Pred. No. 4.6e-137;
  Matches 630; Conservative 0; Mismatches 121; Indels 3; Gaps 1;

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Db 1158 -TACGGTAGTAGTTCCTATACTATGAGTACTCTGGGCCCAAGGAGCACCGTCAACGTCT 1216
QY 546 CCTCAGGTGAGCGGTTCAAGCGGAGGTGGCTCTGGCGTGGCGATCGGATATCGAGC 605
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QY 666 GAGCCAGTGAAGTGTGATAGTTATGGCGATAGTTTATGCACTGGTATCAGCAGAAAC 725
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QY 726 CAGGACAGCCACCAAACTCCTCATCTATCGTGCATCCAACTAGAACTCTGGAGTCCCTG 785
Db 1397 CAGGACAGCCACCAAACTCCTCATCTATCGTGCATCCAACTAGAACTCTGGAGTCCCTG 1456
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Db 1517 CTGATGATCTGCAACCTATTAATCTGCTGCAAGATAGTGGAGATCCGTACACGTTGGAG 1576
QY 906 GGGGACCAAGCTGGAAATAAAACGGGCGCGCG 939
Db 1577 GGGGACCAAGCTGGAGCTGAAGAGGACAGTGGC 1610

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RESULT 7
AF402256 744 bp mRNA linear SYN 12-AUG-2001
LOCUS Synthetic construct single chain antibody HFN7.1 mRNA, partial cds.
DEFINITION
ACCESSION AF402256
VERSION AF402256.1 GI:15149452
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 744)
Kassner,P.D.
Direct Submission
Submitted (24-JUL-2001) Molecular Biology, Pointilliste, 2541
Leghorn Street, Suite #4, Mountain View, CA 94043, USA
JOURNAL
FEATURES
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Best Local Similarity 83.7%; Pred. No. 1.5e-136;
Matches 628; Conservative 0; Mismatches 116; Indels 6; Gaps 1;
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RESULT 8
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LOCUS Sequence 93 from Patent WO0119992.
DEFINITION AX100186
ACCESSION AX100186
VERSION AX100186.1 GI:13539105

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RESULT 10
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LOCUS AX100188 969 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 95 from Patent WO0119992.
ACCESSION AX100188
VERSION AX100188.1 GI:13539106
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Scheiflinger, F., Kerschbaumer, R., Falkner, F. G. and Dörner, F.
TITLE Factor ix/factor ixa antibodies and antibody derivatives
JOURNAL Patent: WO 0119992-A 95 22-MAR-2001;
Baxter Aktiengesellschaft (AT)
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Matches 647; Conservative 0; Mismatches 151; Indels 9; Gaps 1;

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DEFINITION Artificial mRNA for single chain antibody scFv (scFvP25).
ACCESSION Z70562
VERSION Z70562.1 GI:1360013
KEYWORDS heavy chain; light chain; single chain antibody; variable region.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 795)
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Fecker, L., Kaufmann, A., Commandeur, U., Reither, J., Koenig, R. and Burgermeister, W.
Expression of single chain antibody fragments (scFv) specific for
beet necrotic yellow vein virus structural and nonstructural
proteins in Escherichia coli and Nicotiana benthamiana
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 795)
Fecker, L.
TITLE Direct Submission
JOURNAL Submitted (03-APR-1996) Fecker L., Biologische Bundesanstalt fuer
Land- und Forstwirtschaft, Institut fuer
Biochemie/Pflanzenvirologi, Messeweg 11-12, Braunschweig, Germany,
38104
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LOCUS
DEFINITION
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ACCESSION
AF003707
VERSION
AF003707.1 GI:3322218
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
synthetic construct; artificial sequences.
REFERENCE
1 (bases 1 to 687)
Amedorfer, P., Wong, C., Chen, S., Smith, T., Deshpande, S.,
Sheridan, R., Finnern, R. and Marks, J.D.
Molecular characterization of murine humoral immune response to
botulinum neurotoxin type A binding domain as assessed by using
phage antibody libraries
Infect. Immun. 65 (9), 3743-3752 (1997)
JOURNAL
MEDLINE
97427959
PUBMED
9284147
REFERENCE
2 (bases 1 to 687)
Amedorfer, P.
Direct Submission
TITLE
Submitted (13-MAY-1997) Anesthesia, University of California at San
Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
JOURNAL
3 (bases 1 to 687)
Amedorfer, P.
Direct Submission
TITLE
Submitted (16-JUL-1998) Anesthesia, University of California at San
Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
JOURNAL
REMARK
Sequence update by submitter
COMMENT
On Jul 16, 1998 this sequence version replaced gi:2306928.
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Query Match 49.4%; Score 508.4; DB 12; Length 687;
Best Local Similarity 83.8%; Pred. No. 2.8e-127;
Matches 625; Conservative 0; Mismatches 61; Indels 60; Gaps 2;
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Db 662 GGGGGACCAAGCTGGAAATAAAACGG 687

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LOCUS
DEFINITION
Sequence 25 from Patent WO03025018.
ACCESSION
AX739887
VERSION
AX739887.1 GI:30519176
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
synthetic construct; artificial sequences.
REFERENCE
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le Gall, P., Kipriyanov, S., Reusch, U., Moldenhauer, G. and Little, M.
Dimeric and multimeric antigen binding structure
Patent: WO 03025018-A 25 27-MAR-2003;
Affimed Therapeutics AG (DE)
Location/Qualifiers
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QY	197	CAGCAGTCAAGGGCTCAGCTGGTGGCCCTGGGGTCTCAGTGAAGATTTCTGCAAGGGT 256
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QY	257	TCGTGGCTACACATTCACTGATTATGATATGAGCTGGGTGAACAGAGTCATGCAGAGT 316
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QY	317	CTAGAGTGGATTGGACTTATTAGTACTTACTATGCTGATCTCTAGTTTCAACACAGAGTTTC 376
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QY	377	AGGGGCAAGGCCACATGACTGTAGCAAAATCCTCCAAACAAGCTATTATTGGAATCTGCC 436
DB	381	AGGGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCAGAGCTCATGCAACTCAGC 440
QY	437	AGACTGACATCTGAGGATCTGCCATTTATTATTGTCGAAGATCGGATGTTA-----AT 490
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QY	491	TAGCGGTATTACTATGCTTTGACTACTGGGCCAAGGCACATAGCGTCAACCGTCTCTCTCA 550
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QY	551	G-----GTGGAGGGCGTTTCAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAG 604
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QY	725	CCAGGACAGCCACCAAACTCTCATCTATCGTGCATCCAACTAGAGTCTGGAGTCCCT 784
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LOCUS	882 bp	RNA linear SYN 21-OCT-2000
DEFINITION	Synthetic construct for anti-CTV coat protein ScFv antibody.	

GenCore version 5.1.6
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Searched: 4390206 seqs, 2959870667 residues

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Minimum DB seq length: 0

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SUMMARIES

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4	598.8	58.1	927	5	AAF61510 DNA encod
5	594.2	57.7	868	10	ACC57513 Newcastle
6	538	52.2	2190	4	AAF30729 Antibody
7	537.6	52.2	876	4	AAF30734 DNA encod
8	537.4	52.2	969	4	AAF30730 Antibody
9	536.8	52.1	744	10	ADL07528 P. pastor
10	526.2	51.1	1094	3	AAAG0982 Antibody
11	522.6	50.7	925	3	Aaz44206 Murine de
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13	503.4	48.9	1817	8	ACC79607 Plasmid p
14	487.6	47.3	857	13	ADS88776 Nucleotid
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16	483	46.9	993	9	AAAD56799 Chemokine
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20	479.2	46.5	978	4	AAF30728 Anti-FIX/

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38	444	43.1	807	3	AAZ28963	Aaz28963 Anti-Hepa
39	444	43.1	807	13	ADS08281	Ad808281 Human ant
40	439.4	42.7	783	4	AAAC86582	Aac86582 DNA encod
41	439.4	42.7	783	9	ABT43521	Abt43521 scFvSA fu
42	438	42.5	786	13	ADT91212	Adt91212 Single ch
43	435	42.2	906	5	AAAF61513	Aaf61513 DNA encod
44	434.8	42.2	843	2	AAV73323	Aav73323 Human scF
45	434.8	42.2	1452	2	AAV73324	Aav73324 Chimeric

ALIGNMENTS

RESULT 1
AAF61509
ID AAF61509 standard; DNA; 1030 BP.

XX AAF61509;

XX AC

DT 11-SEP-2003 (revised)

DT 25-JUN-2001 (first entry)

XX DNA encoding SNV-env leader/human 7A5-scFv fusion construct.

DE T lymphocyte; antibody; single chain variable antibody; scFv; human;
XX cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
KW acquired immune deficiency syndrome; severe combined immune deficiency;
KW T cell lymphoma; fusion construct; ds.

XX Homo sapiens.

OS Spleen necrosis virus.

OS Chimeric.

XX Key

XX Location/Qualifiers

FT CDS

FT /tag= a

FT /product= "SNV-env leader peptide"

FT /note= "No stop codon given"

FT CDS

FT /tag= b

FT /product= "7A5-scFv"

FT /note= "no stop codon given"

XX DE19946142-A1.

XX 29-MAR-2001.

XX 27-SEP-1999; 99DE-01046142.

XX 27-SEP-1999; 99DE-01046142.

XX (BUND) BUNDESREPUBLIK DEUT PAUL-BHRLLICH-INST.

XX Cichutek K, Engelstaedter M;

XX 29-MAR-2001.
PD 27-SEP-1999; 99DE-01046142.
PF 27-SEP-1999; 99DE-01046142.
XX (BUND) BUNDESREPUBLIK DEUT PAUL-EHRlich-INST.
XX Cichutek K, Engelstaedter M;
XX WPI; 2001-246140/26.
DR P-PSDB; AAB70843.
XX Cell-targeting vector selective for T lymphocytes, useful in gene therapy
PT of e.g. acquired immune deficiency syndrome, encodes a single-chain
PT variable antibody fragment.
XX Claim 1; Fig 4; 18pp; German.
XX This invention describes a novel cell-targeting vector (A) containing a
CC DNA sequence (I) encoding a single-chain variable antibody fragment
CC (scFv). The products of the invention have antiviral, cytostatic and
CC immunostimulant activity and can be used in gene therapy, immunization
CC and diagnosis particularly of T cell-associated diseases, specifically
CC acquired immune deficiency syndrome (AIDS), severe combined immune
CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
CC human B cells, and 1000 fold selectivity over other human cells. A vector
CC designated 7A5 encodes a 329 amino acid single-chain variable antibody
CC fragment, fully defined in the specification. It was used to transform
CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
CC (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
CC carcinoma) cells. After 48 hours, the cells were stained with X-gal to
CC determine transfection. The viral titer (infectious units/ml) was over
CC 1 million for D17, 1 million for C8166 but less than 100 for HeLa,
CC showing the high selectivity for human T cells. This sequence encodes the
CC SNV-env leader/human 7E4-scFv fusion construct used in the construction
CC of novel cell targeting vectors described in the invention. (Updated on
CC 11-SEP-2003 to standardise OS field)
XX SQ Sequence 946 BP; 199 A; 249 C; 276 G; 222 T; 0 U; 0 Other;
Query Match 61.1%; Score 629.2; DB 5; Length 946;
Best Local Similarity 80.2%; Pred. No. 3.5e-148;
Matches 768; Conservative 0; Mismatches 178; Indels 12; Gaps 2;
QY 44 ATGGACTGTCTCACCACCTCCGATCCGCTGAGGGTAAAGTTGACCGAGCAAAATC 103
DB 1 ATGGACTGTCTCACCACCTCCGATCCGCTGAGGGTAAAGTTGACCGAGCAAAATC 60
QY 104 CTAATTTCTCTTGGCTTGGTGGGGTTGGACCACTGCCAGCTTTCGACTGCCGA 163
DB 61 CTAATTTCTCTTGGCTTGGTGGGGTTGGACCACTGCCAGCTTTCGACTGCCGA 120
QY 164 GCGGCCAGCGCGCCATGGCCGAGGTCAAGCTCAGCAGTCAAGGGCTGAGTGGAGG 223
DB 121 GCGGCCAGCGCGCCATGGCCGAGGTCAAGCTCAGCAGTCAAGGGCTGAGTGGAGG 190
QY 224 CTTGGGGTCTCAGTGAAGATTTCTCTGCAAGGGTTCTGGCTTACATCTGATTAAGT 283
DB 181 CTTGGGGTCTCAGTGAAGATTTCTCTGCAAGGGTTCTGGCTTACATCTGATTAAGT 240
QY 284 ATGAGCTGGGTGAACAGAGTCAAGAGCTGAGAGTGGATTTGAGCTATTAGTACT 343
DB 241 ATGAACTGGGTGAAGCTGAGAGTGGATTTGAGTGGATTTGAGCTATTAGTACT 300
QY 344 TACTATGGTATCTCTAGTTACACAGAGGTTCAGGGGCAAGGCCCAATGACTGTAGAC 403
DB 301 TCCGATAGTGAACACTAGTTTAACTCAGAGGTTCAGGACCAAGGCCCACTGACTGTAGAC 360
QY 404 AAATCTCCAAACAGCCTATTGGAACCTTGGCACTGACATCTGAGGATTTCTGCCATT 463

DB 361 AAATCTCCAGCAGCCCTACATGCAACTCAGACGCCCGACATCTGAGGACTCTGCGGTC 420
QY 464 TATTATTGTGCAAGATCGGATGATTAATACGGGTATTACTATGCTTTGAGACTACTGGGCG 523
DB 421 TATTATTGTGCAAGATCTCTTTATGCTAAC---TACCCCTCTCTGTTTACTTACTGGGCG 477
QY 524 CAAGGCACCTACCGGTCAACCGTCTCTCTCAGGTGAGGCGGTTTCAGGGCGAGGTGGCTTCGC 583
DB 478 CAAGGCACCTACCGGTCAACCGTCTCTCTCAGGTGAGGCGGTTTCAGGGCGAGGTGGCTTCGC 537
QY 584 GGTGGCGGATCGGATATCGAGCTCACTCAGTCTCCATCTTCTTTGGCTGTGTCTTAGCG 643
DB 538 GGTGGCGGATCGGATATCGAGCTCACTCAGTCTCCAAACCAACCATGGCTGCATCTCCCGG 597
QY 644 CAGAGGGCCACCATATCTCTGAGAGCCAGTGAAGTGTGATAGTTATGCGCATAGTTTTT 703
DB 598 GAGAAGATCACTATCACCTGAGTGCAGTCCAGTAT-----AAGTTCCATTTAC 648
QY 704 ATGCATCTGGTATCAGCAGAAACCCAGGACAGCCCAAACTCCTCATCTATCTGTCATCC 763
DB 649 TTGCATTTGTTATCAGCAGAAAGCCAGGATTTCTCCCTAAACTCTTGATTTATAGGACATCC 708
QY 764 AACCTAGATCTGGAGTCCCTGCCAGGTTTCAGTGGCAGTGGGCTCAGTCAGACTTCATCT 823
DB 709 AATCTGGCTTCTGGAGTCCAGCTCGCTTCAGTGGCAGTGGGCTCGGGACCTCTTACTCT 768
QY 824 CTCACCATCGATCTCTGTGGAGGAAGATGATGCTGAGTGTATTTACTGTCTGCAAAAGTATG 883
DB 769 CTCACAACTGGCACCATTGAGAGCTGAGATGTTGCCATTTACTCTGAGCAGAGGTAGT 828
QY 884 GAAGATCCGTACACGTTTCGAGGGGGGACCAAGCTGGAATAAAGCGGGCGGCGCATCG 943
DB 829 AGTATACCGTACACGTTTCGAGGGGGGACCAAGCTGGAATAAAGCGGGCGGCGCATCG 888
QY 944 GGTCTCGGGGGGGGCTGCTGCTGGTGGTCTGCTGGTGGTGGTCTGCTGGTGGTGGT 1001
DB 889 GGTCTCGGGGGGGGCTGCTGCTGGTGGTGGTCTGCTGGTGGTGGTCTGCTGGTGGTGGT 946
RESULT 4
AAF61510
ID AAF61510 standard; DNA; 927 BP.
XX
AC AAF61510;
XX
DT 11-SEP-2003 (revised)
DT 25-JUN-2001 (first entry)
XX
DE DNA encoding SNV-env leader/human K6-scFv fusion construct.
XX T lymphocyte; antibody; single chain variable antibody; scFv; human;
KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
KW acquired immune deficiency syndrome; severe combined immune deficiency;
KW T cell lymphoma; fusion construct; ds.
XX Homo sapiens.
OS Spleen necrosis virus.
OS Chimeric.
XX
FH Key Location/Qualifiers
CDS 1..135
FT /tag= a
FT /product= "SNV-env leader peptide"
FT /notes= "No stop codon given"
FT 136..927
CDS /tag= b
FT /product= "K6-scFv"
FT /notes= "no stop codon given"
XX /partial
PN DE19946142-Al.
XX

PD	29-MAR-2001.	QY	464	TATTATTGTCAGATCGGATGCTAATACGGGTATTATCTATCTGTTGGACTACTGGGC	523
XX		Db	421	TATTACTGTGCAAGAAAGG-----GCTATGCTATGGACTACTGGGC	462
PF	27-SEP-1999; 99DE-01046142.	QY	524	CAAGGCACATACGGTCAACCGTCTCTCAGGTGGAGCGGTTTCAGCGGAGGTGGCTCTGGC	583
XX		Db	463	CAAGGCACCAACGTCACCGTCTCTCAGGTGGATGCGGTTTCAGCGGAGGTGGCTCTGGC	522
PA	(BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.	QY	584	GGTGGCGGATCGGATATCGAGTCACTCAGTCTCCATCTCTTTGGTGTGTCTCTAGGG	643
XX	Cichutek K, Engelstaedter M;	Db	523	GGTGGCGGATCGGATATCGAGTCACTCAGTCTCCATCTCTTTGGTGTGTCTCTAGGG	582
XX	WPI; 2001-246140/26.	QY	644	CAGAGGCCACCATATCTCTGCAGAGCCAGTGAAGTGTGATAGTTATGCGCGATGTTT	703
DR	P-PSDB; AAB70841.	Db	583	GAGAAGGTACCATGACCTGCGAGTCCAGCTCAAGTAT-----AAGTTAC	627
XX	Cell-targeting vector selective for T lymphocytes, useful in gene therapy	QY	704	ATGCACTGGTATCAGCAGAAACAGGACAGCCACCAAACTCTCTATCTATCTGTCATCC	763
PT	of e.g. acquired immune deficiency syndrome, encodes a single-chain	Db	628	ATGCACTGGTATCAGCAGAAACAGGACAGCCACCAAACTCTCTATCTATCTGTCATCC	687
PT	variable antibody fragment.	QY	764	AACCTAGAATCTGGAGTCCCTGCCAGGTTCAGTGGAGTGGTCTCAGTCTGAGTCACT	823
XX	Claim 1; Fig 2; 18pp; German.	Db	688	AACTGGCTTCTGGAGTCCCTGCTCGCTTCACTGAGTGGGTCTGGGACCTCTTATCT	747
XX	This invention describes a novel cell-targeting vector (A) containing a	QY	824	CTCACCATCGATCCTCTGCGAGGAAGATGATGCTGCACTGTTATCTCTGCTGCAAGTATG	883
CC	DNA sequence (I) encoding a single-chain variable antibody fragment	Db	748	CTCCCAATCAGCAGATGAGGCTGAAGATGCTGCCACTTATTACTGCCATCAGCGAGT	807
CC	(scFv). The products of the invention have antiviral, cytostatic and	QY	884	GAAGATCCGTACACGTTCCGAGGGGGGAGCAAGCTGGAATAAAACGGCGCGCATCG	943
CC	immunostimulant activity and can be used in gene therapy, immunization	Db	808	AGTTACCATGAGCGTTCCGTTGGAGGAGCAACAGCTGGAATAAAACGGCGCGCATCG	867
CC	and diagnosis particularly of T cell-associated diseases, specifically	QY	944	GGCTCCGGGGGGGGTCTGGTGTGTGTCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1003
CC	acquired immune deficiency syndrome (AIDS), severe combined immune	Db	868	GGCTCCGGGGGGGGTCTGGT	927
CC	deficiency (SCID) or T cell lymphoma. (A) target T cells, independently				
CC	of the CD4 receptor, with high selectivity, 4-5 fold selectivity over				
CC	human B cells, and 100 fold selectivity over other human cells. A vector				
CC	designated 7A5 encodes a 329 amino acid single-chain variable antibody				
CC	fragment, fully defined in the specification. It was used to transform				
CC	D17 (canine osteosarcoma cells susceptible to spleen necrosis virus				
CC	(SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical				
CC	carcinoma) cells. After 48 hours, the cells were stained with X-gal to				
CC	determine transfection. The viral titer (infectious units/ml) was over				
CC	1 million for D17, 1 million for C8166 but less than 100 for HeLa,				
CC	showing the high selectivity for human T cells. This sequence encodes the				
CC	SNV-env leader/human K6-scFv fusion construct used in the construction of				
CC	novel cell targeting vectors described in the invention. (Updated on 11-				
CC	SEP-2003 to standardise OS field)				
XX					
SQ	Sequence 927 BP; 205 A; 238 C; 277 G; 207 T; 0 U; 0 Other;				
	Query Match				
	Best Local Similarity 58.1%; Score 598.8; DB 5; Length 927;				
	Matches 755; Conservative 0; Mismatches 172; Indels 33; Gaps 2;				
QY	44 ATGCACTGCTCACCACCTCCGATCCGCTGAGGGTAAAGTTGACCGAGCAGCAAAATC 103				
Db	1 ATGCACTGCTCACCACCTCCGATCCGCTGAGGGTAAAGTTGACCGAGCAGCAAAATC 60				
QY	104 CTAAATTCCTTGTGGCTTGGTGGGGTGGGACCACTGCCAAGTTTCGACTGCCGA 163				
Db	61 CTAAATTCCTTGTGGCTTGGTGGGGTGGGACCACTGCCAAGTTTCGACTGCCGA 120				
QY	164 GCGGCCCGAGCGGCCGAGGTCAGCTCAGCAGTCAAGCTGAGCTGGTGGAGG 223				
Db	121 GCGGCCCGAGCGGCCGAGGTCAGCTCAGCAGTCAAGCTGAGCTGGTGGAGG 180				
QY	224 CTGGGGTCTCAGTGAAGATTTCTGCAAGGGTCTGGCTACACATTCATGATATGTT 283				
Db	181 CTGGGGTCTCAGTGAATCTGCTTCAAGGGTCTGGCTACACATTCATGATATGTT 240				
QY	284 ATGAGCTGGGTGAACAGAGTATGCAAGAGTCTAGTGGATTTGAGCTATTAGTACT 343				
Db	241 ATGAGCTGGGTGAACAGAGTCTAGTGGATTTGAGCTATTAGTACT 300				
QY	344 TACTATGTGATCTAGTTACACAGAGGTTCAAGGGCAAGCCCAATGCTGTAGAC 403				
Db	301 GTTGTAGTTTACTTAACATCAATCAAACTTCAAGGGCAAGCCCAATGCTGTAGAC 360				
QY	404 AAATCTCCACACAGCTATTGGAACTTGCAGACTGACATCTCAGGATTTCTGCCATT 463				
Db	361 AAGTCTCCACACAGCTATTGGAACTTGCAGACTGACATCTCAGGATTTCTGCCATT 420				
	RESULT 5				
	ACC57513				
ID	ACC57513 standard; cdNA; 868 BP.				
XX	AC	ACC57513;			
XX	AC	ACC57513;			
DT	11-AUG-2003 (first entry)				
XX	Newcastle disease virus F protein scFv coding sequence.				
DE	Newcastle disease virus; NDV; F protein; scFv; antibody; vaccine; tumour;				
KW	Newcastle disease virus; NDV; F protein; scFv; antibody; vaccine; tumour;				
KW	antitumour; mouse; gene; ss.				
XX	Mus sp.				
OS					
FT	Key	Location/Qualifiers			
FT	CDS	1..868			
FT		/tag- a			
FT		/partial			
FT		/product= "NDV(F) scFv"			
FT		/transl_except= (pos:821..826,aa:Ala-Ala-Ala-Gly)			
FT		/transl_except= (pos:4..7,aa:Lys)			
FT		/note= "this codon has an apparent 1 nucleotide insertion			
FT		which alters the reading frame; there is no start or stop			
FT		codon"			
XX					
PN	EP1275724-A1.				
XX					
PD	15-JAN-2003.				
XX					
PF	10-JUL-2001; 2001EP-00116847.				
XX					
PR	10-JUL-2001; 2001EP-00116847.				
XX					
PA	(SCH/) SCHIRRMACHER V.				

CC (VH) and light (VL) chain variable regions of antibody 8860 joined by an
CC artificial, flexible linker peptide; Escherichia coli alkaline
CC phosphatase; and a C-terminal 6His affinity tail. The DNA was used in the
CC construction of a miniantibody construct (see AAF30730), which was used
CC as negative control in determination of Factor VIII (FVIII)-like activity
CC of a 198/B1 miniantibody. 198/B1 is an example of anti-human Factor IX
CC (FIX)/activated Factor IX (FIXa) antibodies of the invention. Anti-
CC FIX/FIXa antibodies and their derivatives have FVIIIa cofactor or FIXa
CC activating activity. Administration leads to an increase in the
CC procoagulant activity of FIXa, even in the presence of FVIIIa inhibitors.
CC This allows for rapid blood coagulation even in the absence of FVIII or
CC FVIIIa, and in the case of FVIII inhibitor patients. The antibodies and
CC derivatives are used in a claimed pharmaceutical composition for treating
CC patients with blood coagulation disorders, especially haemophilia A and
CC haemorrhagic diathesis. The scFv-alkaline phosphatase was expressed in E.
CC coli. It exhibited no FVIII-like activity
XX
SQ Sequence 2190 BP; 549 A; 579 C; 606 G; 456 T; 0 U; 0 Other;
Query Match 52.2%; Score 538; DB 4; Length 2190;
Best Local Similarity 80.3%; Pred. No. 3.9e-125;
Matches 647; Conservative 0; Mismatches 150; Indels 9; Gaps 1;
QY 137 ACCACTGCCGAAGTTTCGACTGCCGAGCGCCGAGCGCCCATGCCGAGGTCAAAGCTG 196
DB 19 ACGGACGCGCTGGATTGTTTACTCGCGGCCGAGCGGCCATGCCGAGGTTTCAGCTT 78
QY 197 CAGCAGTACAGGGCTGAGCTGGTGAGCGCTGAGCGCTGAGTGAAGATTTCCTGCAAGGCT 256
DB 79 CAGCAGTCTGGACCTGAGCTGGTGAAGCGCGGCGCTCAGTGAAGATTTCCTGCAAGCT 138
QY 257 TCTGGCTACACATTCTACTGATTGATGATGAGTGGTGAACAGAGTCAATGCAAGCT 316
DB 139 TCTGGCTACGCAATTCAGTCTGATGATGAGTGGTGAACAGAGGCTGACAGGCT 198
QY 317 CTAGAGTGGATTGCACTTATAGTCTTACTATGTTGATCTAGTTTACAACAGAGGTTCT 376
DB 199 CTGAGTGGATTGCAAGGATTATCTGGAATGGAGATCTAATCTACATGGGAAGTTCT 258
QY 377 AAGGCAAGGCCCAATAGTCTGAGCAAAATCTTCCAACACAGCCTATTGGAAGTTGCC 436
DB 259 AAGGCAAGGCCCACTGACTGTCAGACAAATCTCCAGCAGACGCTACATGCACTCAGC 318
QY 437 AGACTGACATCTGAGGATCTGCAATTTATTGTCAGATCGGATGGTAATTACGGG 496
DB 319 AGCTGACCTCTGTGACTCTGCGGCTATTCTGTGCA-----GATGGTAACGTA 369
QY 497 TATTACTATGCTTTGGACTACTGGGCGCAAGGCACTACGTCACCGTCTCCTCAGGTGGA 556
DB 370 TATTACTATGCTATGCACTACTGGGCTCAAGNACCTCAGTCACCGTCTCCTCAGGTGGA 429
QY 557 GCGGTTTCAGGCGGAGGTGGCTCTGCGGTTGCGGATTCGGATATCGAGCTCACTCAGTCT 616
DB 430 GCGGTTTCAGGTGGCGCGCTCTGCGGTTGCGGATTCGCAATTTGTTCTCACCCAGTCT 489
QY 617 CCATCTCTCTTGGCTGTCTCTAGGGCAGAGGGCCACCATTCTCTGAGAGCCAGTGAA 676
DB 490 CTGCTCTCTTCTAGCTATCTCTGCGGCGAGAGGGCCACCATTCTCTGAGGGCCAGCAAA 549
QY 677 AGTGTGTAGTATTATGGCATAGTTTATGCACTGCTATCAGCAGAAACACAGGACAGCCA 736
DB 550 AGTGTGAGTACATCTGGCTATAGTTATATGCACTGGTATCAACAGAAACAGGACAGCCA 609
QY 737 CCCAAATCTCTCATCTATCGTGATCCAACTAGAAATCTGGAGTCCCTGCCAGGTTTCAGT 796
DB 610 CCCAAATCTCTCATCTATCTTGATCCAACTAGAAATCTGGGTCCTGCCAGGTTTCAGT 669
QY 797 GGCAGTGGGTCTGAGTCAGACTTCACTCAACATCGATCTCTGTGAGGAAGATGATGCT 856
DB 670 GGCAGTGGGTCTGGGACAGACTTCACTCAACATCATCTCTGTGAGGAGGAGGATGCT 729
QY 857 GCAGTGTATTACTGTCTGCAAGTATGGAAGATCCGTACACGTTCTGAGGGGGGACCAAG 916

Db 730 GCAACCTATTACTGTCTGACACAGTAGGAGCTTCTCTCGGACGTTCTGGTGGAGGCCAAG 789
QY 917 CTGGAATAAATCAACGGCGCGCGGCATC 942
Db 790 CTGGAATAAATCAACGGCGCGCGGCAGC 815
RESULT 7
AAF30734
ID AAF30734 standard; DNA; 876 BP.
XX
AC AAF30734;
XX
DT 21-JUN-2001 (first entry)
XX
DE DNA encoding antibody 8860 scFv with c-myc-tag.
XX
KW Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse; myc-tag;
KW ds.
XX
OS Mus musculus.
OS Synthetic.
OS Escherichia coli.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 1..876
FT sig_peptide /*tag= a
FT mat_peptide /*tag= b
FT /*tag= 67..873
FT /*tag= c
XX
PN WO200119992-A2.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-EP008936.
XX
PR 14-SEP-1999; 99AT-00001576.
XX
PA (BAXT) BAXTER AG.
XX
PI Scheiflinger F, Kerschbaumer R, Falkner F, Dörner F;
XX
XX WPI; 2001-290358/30.
XX P-PSDB; AAB20443.
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
XX increasing amidolytic activity of factor IXa, and for treating blood
XX coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX
XX Example 18; Fig 35; 138pp; English.
XX
XX The present sequence is that of DNA encoding a fusion protein (see
XX AAB20443) comprising (from the N-terminal end): a PelB leader sequence; a
XX single chain Fv (scFv) derivative of antibody 8860 comprising the heavy
XX (VH) and light (VL) chain variable regions of 8860 joined by an
XX artificial, flexible linker peptide; a Myc-tag and a C-terminal 6His
XX affinity tail. The fusion protein was expressed in Escherichia coli from
XX vector pMyHis6. The construct was used as a negative control to
XX determine the Factor VIII (FVIII)-like activity of a 198/B1 antibody scFv
XX fragment (see AAB20442) also expressed from pMyHis6. 198/B1 (clone AB2)
XX is an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)
XX antibodies of the invention. Anti-FIX/FIXa antibodies and their
XX derivatives, including scFv fragments, have FVIIIa cofactor activity or
XX FIXa activating activity. Administration leads to an increase in the
XX procoagulant activity of FIXa, even in the presence of FVIIIa inhibitors.
XX This allows for rapid blood coagulation even in the absence of FVIII or
XX FVIIIa, and in the case of FVIII inhibitor patients. The antibodies and
XX derivatives are used in a claimed pharmaceutical composition for treating

CC	patients with blood coagulation disorders, especially haemophilia A and		
XX	haemorrhagic diathesis		
SQ	Sequence 876 BP; 211 A; 233 C; 239 G; 193 T; 0 U; 0 Other;		
Query Match	52.2%; Score 537.6; DB 4; Length 876;		
Best Local Similarity	80.3%; Pred. No. 3.8e-125;		
Matches	646; Conservative 0; Mismatches 149; Indels 9; Gaps 1;		
QY	137 ACCACTGCCGAGTTTCGACTGCCAGCGGCCAGCGGCCCATGCGGAGGTCAAGCTG 196	XX	Antibody 8860 bivalent miniantibody DNA.
Db	19 ACGGCAGCCGCTGGATTTATTACTCGCGGCCAGCCGCGCCATGCCGAGGTTCAGCTT 78	DE	
QY	197 CAGCAGTCAGGGCTCAGCTGGTGAGCGCTTGCGGTCTCAGTGAAGATTTCCTCAAGGCT 256	XX	Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant;
Db	79 CAGCAGTCGACCTGAGCTGGTGAGCCGGGGCTCAGTGAAGATTTCCTGCAAGCT 138	KW	Factor VIII cofactor; blood coagulation disorder; haemophilia A;
QY	257 TCTGGCTACACATCTCACTGATTAATGATGAGCTGGGTGAACAGAGTCATGCAAGAGT 316	KW	haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
Db	139 TCTGGCTACGATTCAGTAGCTCTTGGATGAACCTGGGTGAAGCAGAGGCTGGACAGGT 198	KW	bivalent antibody; p8860-Zip#1.2; ds.
QY	317 CTAGAGTGGATTGGACTTATTAGTACTTACTATGGTGTATCCTAGTTTACAACAGAGTTTC 376	OS	Mus musculus.
Db	199 CTTGAGTGGATTGGACGGATTTTACTCTGGAATGAGATACTAACTACAAATGGGAAGTTC 258	OS	Synthetic.
QY	377 AAGGGCAAGGCCACAATGACTGTAGACAAATCTCCAACACAGCCTATTTCGAACTTGC 436	OS	Escherichia coli.
Db	259 AAGGGCAAGGCCACATGACTGACAGACAAATCTCCAGCACAGCCTACATGACGTGAG 318	XX	Chimeric.
QY	437 AGACTGACATCTGAGGATCTGCCATTTTATTATTGTGCAAGATCGGATGGTAAATTACGGG 496	PH	Location/Qualifiers
Db	319 AGCCTGACCTCTGTGACTCTGGGTCTATTCTGTGCA-----GATGGTAAACGTA 369	FT	1..969
QY	497 TATTACTATGCTTTGAGACTACTGGGGCCAAAGGCACTACGGTCACTCTCTCAGGTGGA 556	CDS	/*tag= a
Db	370 TATTACTATGCTATGACTACTGGGGTCAAGGAACCTCAGTCACTCTCTCAGGTGGA 429	FT	sig_peptide
QY	557 GGCGGTTTCAGGCGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAGTCACTCAGTCT 616	FT	1..86
Db	430 GGCGGTTTCAGTGGCGCGCTCTGGCGGTGGCGGATCGCAATTGTTCTCACCAGTCT 489	FT	/*tag= b
QY	617 CCATCTCTTTGGCTGTGTCTTAGGGCAGAGGCCACCATATPCCTGCAGAGCCAGTGAA 676	FT	/note= "PelB leader sequence"
Db	490 CTTGCTCTCTTAGCTGTATCTCTGGGCGAGAGGCCACCATCTCATGCGAGGCCAGCAA 549	FT	67..966
QY	677 AGTGTGATAGTTATGGCGATGTTTATGCACTGGTATCAGAGAAACCGAGACAGCCA 736	PN	WO200119992-A2.
Db	550 AGTGTGATGATCATCTGGCTATATATGCACTGGTATCAACAGAAACCGAGACAGCCA 609	XX	22-MAR-2001.
QY	737 CCCAAACTCTCATCTATCTGTCATCCAACTAGATCTGGAGTCTCTCCAGGTTTCAGT 796	XX	13-SEP-2000; 2000WO-EP008936.
Db	610 CCCAAACTCTCATCTATCTTGATCCAACTAGATCTGGGTCTCTCCAGGTTTCAGT 669	XX	14-SEP-1999; 99AT-00001576.
QY	797 GGAGTGGGTCTGAGTCAGACTTCACTCTCAATCATGCTCTCTGAGGAAGATGATGCT 856	XX	(BAXT) BAXTER AG.
Db	670 GGAGTGGGTCTGGGACAGACTTCACCTCAACATCATCTCTGAGGAGGAGGATGCT 729	PI	Scheiflinger F, Kerschbaumer R, Falkner F, Dorner F;
QY	857 GCAGTGTATTACTGTCTGCAAGTATGGAAGATCCGTACACGTTCCGGGGGGGACCAAG 916	XX	WPI; 2001-290358/30.
Db	730 GCAACCTATTACTGTGAGCACATAGGAGCTTCTCTGGACGTTTCGTTGAGGACCAAG 789	DR	P-PSDB; AAB20440.
QY	917 CTGGAATAAAACGGGCGGCCGCA 940	XX	New factor IX/factor IXa antibodies and their derivatives useful for
Db	790 CTGGAATAAAACGGGCGGCCGCA 813	PT	increasing amidolytic activity of factor IXa, and for treating blood
RESULT 8		PT	coagulation disorders such as hemophilia A and hemorrhagic diathesis.
AAF30730		PS	Example 16; Fig 30; 138pp; English.
ID	AAF30730 standard; DNA; 969 BP.	CC	The present sequence is that of the coding region of plasmid p8860-
XX		CC	Zip#1.2 encoding a bivalent miniantibody (see AAB20440) comprising the
AC	AAF30730;	CC	single chain Fv (scFv) fragment of antibody 8860 fused to an amphipathic
XX		CC	helical structure. The plasmid was obtained by inserting 8860 scFv DNA
DT	21-JUN-2001 (first entry)	CC	into vector p2ipl. The construct was used as negative control in
		CC	examination of the factor VIII (FVIII)-like activity of an antibody
		CC	193/B1 miniantibody (see AAB20438). 193/B1 is an example of anti-human
		CC	Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the invention.
		CC	Anti-FIX/FIXa antibodies and their derivatives have FVIIIa cofactor
		CC	activity or FIXa activating activity. Administration leads to an increase
		CC	in the procoagulant activity of FIXa, even in the presence of FVIIIa
		CC	inhibitors. This allows for rapid blood coagulation even in the absence
		CC	of FVIII or FVIIIa, and in the case of FVIII inhibitor patients. The
		CC	antibodies and derivatives are used in a claimed pharmaceutical
		CC	composition for treating patients with blood coagulation disorders,
		CC	especially haemophilia A and haemorrhagic diathesis. The present bivalent
		CC	miniantibody exhibited no FVIII-like activity
		XX	
		SQ	Sequence 969 BP; 233 A; 257 C; 264 G; 215 T; 0 U; 0 Other;
		Query Match	52.2%; Score 537.4; DB 4; Length 969;
		Best Local Similarity	80.2%; Pred. No. 4.4e-125;
		Matches	647; Conservative 0; Mismatches 151; Indels 9; Gaps 1;
		QY	137 ACCACTGCCGAGTTTCGACTGCCAGCGGCCAGCGGCCCATGCGGAGGTCAAGCTG 196
		Db	19 ACGGCAGCCGCTGGATTTATTACTCGCGGCCAGCCGCGCCATGCCGAGGTTCAGCTT 78
		QY	197 CAGCAGTCAGGGCTCAGCTGGTGAGCGCTTGCGGTCTCAGTGAAGATTTCCTCAAGGCT 256

Db 79 CAGCAGTCTGGACCTGAGCTGGTGAAGCCGGGGCCCTCAGTGAAGATTTCTCTGCAAGCT 138
Qy 257 TCTGGCTACACATTCACCTGATTATGGTATGAGCTGGGTGAAACAGAGTCAATGCAAGAGT 316
Db 139 TCTGGCTACGCAATTCAGTAGCTCTGTGATGAATGGGTGAAGCAGAGGCTTGGACAGGGT 198
Qy 317 CTAGAGTGGATTGGACTTATTTAGTACTTACTATGTTGATCTCTAGTATCAACACGAGGTTT 376
Db 199 CTTGAGTGGATTGGACGGATTTATCTTGGAAATGGAGATTAATACTAATGGAAGTTT 258
Qy 377 AAGGGCAAGGCCCAATGACTGTAGACAAATTCCTCCAACACAGCCTATTTTGGAACTTGGC 436
Db 259 AAGGGCAAGGCCCACTGACTGTGACAGAAATTCCTCCAGCACAGCCTACATGCACTCAGC 318
Qy 437 AGACTGCATCTGAGGATTCGCAATTTATATGTCGAAGATCGGATGTAATACGGG 496
Db 319 AGCTGACCTCTTGGACTCTGGGCTCTTCTTCTGTGCA-----GATGGTAACTGA 369
Qy 497 TATTACTATCTTTGGACTACTGGGGCAAGGCACTACGGTCAACCGTCTCTCAGGTGGA 556
Db 370 TATTACTATCTTGGACTACTGGGGTCAAGGAACCTCAGTCAACCGTCTCTCAGGTGGA 429
Qy 557 GCGGTTTCAAGCGAGGTGCTCTGGCGGTGGCGGATCGGATATCGAGCTCACTCAGTCT 616
Db 430 GCGGTTTCAAGCGAGGTGCTCTGGCGGTGGCGGATCGGATATCGGATATCGGATATCGG 489
Qy 617 CCATCTCTTTGGCTGTCTTAGGGCAGAGGCCACCATATCTCTCAGAGCCAGTGAA 676
Db 490 CTTGCTCTCTTAGCTGTATCTCTGGGGCAGAGGCCACCATCTCTCAGAGGCCAGCAAA 549
Qy 677 AGTGTGATAGTATGCGGATAGTTTATGCACTGGTATCAGCAGAAACACGAGCACCCA 736
Db 550 AGTGTGATAGTATGCGGATAGTTTATGCACTGGTATCAGCAGAAACACGAGCACCCA 609
Qy 737 CCCAAATCTCTATCTATCTGATCAACCACTAGAGTCTGGAGTCCCTGCGAGGTTTCAGT 796
Db 610 CCCAAATCTCTATCTATCTGATCAACCACTAGAGTCTGGAGTCCCTGCGAGGTTTCAGT 669
Qy 797 GGCAGTGGGTCTGAGTCAGACTTCACTCTCACCATCGATCTCTGAGGAGGAATGATGCT 856
Db 670 GGCAGTGGGTCTGAGTCAGACTTCACTCTCACCATCGATCTCTGAGGAGGAGGATGCT 729
Qy 857 GCAGTGTATTACTCTGCAAGTATGGAAGATCCGTACAGTCTCGAGGGGGGACCAAG 916
Db 730 GCAACCTATTACTCTGACACAGTAGGAGCTTCTCTCGAGCTTCTCGGTGAGGACCAAG 789
Qy 917 CTGGAATAAAACGGGCGCGCATCG 943
Db 790 CTGGAATAAAACGGGCGCGCATCG 816

RESULT 9

ADL07528

ID ADL07528 standard; DNA; 744 BP.

XX AC ADL07528;

XX DT 06-MAY-2004 (first entry)

XX DE P. pastoris ScFv-43 DNA.

XX KW scFv-LDP; ScFv-43; type IV collagenase; single-chain Fv fragment;

XX KM Lidyamycin agon protein; LDP; methanol nourishing yeast; vascularisation;

XX KW tumour; invasive metastasis; antibody; ds.

XX OS Pichia pastoris.

XX CN1403577-A.

XX PD 19-MAR-2003.

XX PF 06-SEP-2001; 2001CN-00131299.

XX

PR 06-SEP-2001; 2001CN-00131299.

XX (MEDI-) INST MEDICINAL BIOTECHNOLOGY CHINESE ACA.

XX Zhen Y, Tang Y;

XX WPI; 2003-505669/48.

XX Fusion protein of type IV collagenase resistant single chain antibody and

XX Lidyamycin agon protein.

XX Disclosure; SEQ ID NO 1; 18pp; Chinese.

XX The invention relates to the construction of one small fusion protein

XX scFv-LDP by DNA molecular recombination technology and gene engineering

XX technology to constitute the fusion gene of type IV collagenase resistant

XX single-chain Fv fragment, (scFv) gene and Lidyamycin agon protein (LDP).

XX The fusion gene is expressed in methanol nourishing yeast Pichia pastoris

XX and the expressed fusion protein has its binding capacity for antigen

XX type IV collagenase maintained and has inhibits vascularisation of chick

XX embryo allantois membrane. The fusion protein may also function as a

XX double-function small monoclonal antibody guide medicine with the

XX activity of killing tumour cells and of inhibiting invasive metastasis.

XX The present sequence is the Pichia pastoris ScFv-43 DNA.

XX Sequence 744 BP; 179 A; 175 C; 216 G; 174 T; 0 U; 0 Other;

XX Query Match 52.1%; Score 536.8; DB 10; Length 744;

XX Best Local Similarity 83.2%; Pred. No. 5.8e-125;

XX Matches 626; Conservative 0; Mismatches 117; Indels 9; Gaps 1;

Qy 179 ATGCGCGAGTCAAGCTGCAGCAGTCAAGGCGCTCAGCTGGTGGCTGGCTCTCAGTG 238

Db 1 ATGCGCGCGAGTCAAGCTGCAGCAGTCTGGAACCTGGAAGCTTGGGCTTCAAGTG 60

Qy 239 AAGATTTCTGCAAGGCTTCTGCTACACATTCACATGATTGATGATGATGATGATGATG 298

Db 61 AAGTTGCTTGCAGGCTTCTGCTACATCTTCAAGTTATGATATGATATGATATGATATG 120

Qy 299 CAGAGTCATGCAAGAGTCTAGAGTGGATTTGGAATTATTTAGTACTTACTATGATGATCT 358

Db 121 CAGAGCTGCAACAGGAGTCTGATGATTTGATTTGATTTGATTTGATTTGATTTGATTT 180

Qy 359 AGTTACACAGAGGTTCAAGGCAAGGCCACATGATCTGATAGACAAATCTCCACACA 418

Db 181 GAATACAAATGAGAAGTTCAAGGCGAGGCCACATGATGATAGACAAATCTCCACACA 240

Qy 419 GCCTATTGGAACTTGCAGACTGACATCTGAGGATTTGCCATTTTATTTATTTGTCAGA 478

Db 241 GCCTATTGGAGCTCCTAGGCTGACATCTGAGGATTTGCTGCTATTTTCTGCTGCTAGA 300

Qy 479 TCGGATGGTAAATTAACGGGTATTTACTATGCTTTGGACTTCTGGGCGCAAGGCACCTAC 538

Db 301 GGGGACTACTATAGGCGCTA-----CTTTGACTTTGTTGGGCGCAAGGCACCGTTC 351

Qy 539 ACCGTCTCTCAGGTGAGCGGTTTCAAGGCGAGGTGGCTCTGCGGCTGCGGATCCGAT 598

Db 352 ACCGTCTCTCAGGTGAGCGGTTTCAAGGCGAGGTGGCTCTGCGGCTGCGGATCCGAC 411

Qy 599 ATCGAGCTCACTCAGTCTCCATCTTCTTGGCTGTGTCTCTAGGCGAGAGGCCACCAT 658

Db 412 ATCGAGCTCACTCAGTCTCCATCTTCTTGGCTGTGTCTCTAGGCGAGAGGCCACCAT 471

Qy 659 TCCTGCGAGGCCAGTGAAGTGTGTAGTATGATGATGATGATGATGATGATGATGATGATG 718

Db 472 TCCTGCGAGGCCAGTGAAGTGTGTAGTATGATGATGATGATGATGATGATGATGATG 531

Qy 719 CAGAAACACAGGACAGCCACCCAACTCCTCATCTATGTCGATCCCAACCTAGATATCTGA 778

Db 532 CAGAAACACAGGACAGCCACCCAACTCCTCATCTATCTTGCACCAACCTAGATATCTGG 591

Qy 779 GTCCCTGCCAGGTTCAAGTGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 838

Db 592 GTCCCTGCCAGGTTCACTAGTGCAGTGGGTCTAGGACAAATTCACCTCACCATTGATCCT 651
QY 839 GTGAGGAGATGATGCTGCAGTGTATTACTGCTGCAAAAGTATGGAAGATCCGTACACG 898
Db 652 GTGAGGCTGATGATGCTGCAACTATTACTGTGACCAAAATTAAGAGATCCGTACACG 711
QY 899 TTCCGAGGGGGGACCAAGCTGGAATAAACAACG 930
Db 712 TTCCGAGGGGGGACCAAGCTGGAATAAACAACG 743

RESULT 10
AAA60982
ID AAA60982 standard; DNA; 1094 BP.
XX
AC AAA60982;
XX
DT 08-NOV-2000 (first entry)
DE
XX Antibody nucleotide sequence.
DE Lida-protein; LDP; Lida-chromophore; LDC; antibody; lidamycin;
KW antibiotic; anticancer; tumour; cancer; ds.
XX Synthetic.
XX CN1251840-A.
XX PD 03-MAY-2000.
XX PF 13-OCT-1999; 99CN-00121668.
XX PR 13-OCT-1999; 99CN-00121668.
XX PA (MEDI-) INST MEDICINAL BIOTECHNOLOGY CHINESE ACA.
XX PI Zhen Y, Li S, Jiang M;
XX WPI; 2000-432052/38.
XX DR
XX Constitutive fusion protein of ridamycin as anticancer antibiotic and
PT single-chain antibody.
PS Disclosure; Page 2-3; 18pp; Chinese.
XX
CC The present invention describes a fusion protein, designated Lidamycin,
CC composed of Lida-protein (LDP) and Lida-chromophore (LDC), which acts as
CC an anticancer antibiotic and single-chain antibody. LDP and LDC are
CC joined via non-covalent bonds and can be splitted and recombined. A
CC single-chain antibody scFv can specifically join with IV-type collagenase
CC and can suppress its activity and in order to increase the permeability
CC of medicine to capillary tubes and the penetrability to real tumour, DNA
CC recombination and molecular recombination are used to prepare new-type
CC constitutive fusion protein LDM-Fv of anticancer targeting medicine
CC Lidamycin and single-chain antibody. Its molecular weight is about 37kDa.
CC It has the activity to inhibit IV-type collagenase and strong intrusion-
CC resistance kill action to cancer cells. It may be an ideal clinic
CC medicine. The present sequence represents an antibody nucleotide sequence
CC given in the exemplification of the present invention
XX
SQ Sequence 1094 BP; 230 A; 312 C; 325 G; 227 T; 0 U; 0 Other;

Query Match 51.1%; Score 526.2; DB 3; Length 1094;
Best Local Similarity 82.8%; Pred. No. 3e-122; Indels 21; Gaps 1;
Matches 622; Conservative 0; Mismatches 108;
QY 179 ATGCCGAGGTCAAGCTGCAGCAGTCAAGGGGCTGAGCTGGTGGGCTTCAGTGC 238
Db 1 ATGCCGAGGTCAAGCTGCAGCAGTCTGGACCTGAACCTGGTGAAGCTGGGGCTTTAGTG 60
QY 239 AAGATTCTCGAAGGGTCTGGCTACACATTCACTGATTATGATAGCTGGGTGAAA 298
Db 61 AAAATATCTCGAAGGCTTCTGGTTACACCTTCACAGACTACGATATAAACTGGTGAAG 120

QY 299 CAGAGTCATGCAAAAGAGTCTAGAGTGGATTGGACTTATTAGTACTTATCTATGGTATCCT 358
Db 121 CAGAGCCCTGGACAGGACTTGGATGGATTGGATGGATTATCCTCGGAGATGGTAGTGCT 180
QY 359 AGTTACAAACAGAGGTTCAAGGGCAAGGCCAACATGACTGTAGACAAATCTCTCCAAACA 418
Db 181 AAGTACAATGAGAAGTTCAAGGGCAAGGCCAACATGACTGTAGACAAATCTCTCCAAACA 240
QY 419 GCCTATTGGAACTTGCAGACTGACATCTGAGGATCTGCCATTTATTATTGTGCAAGA 478
Db 241 GCCTACATGACGTCAGCAGCCTGACTTCTGAGAACTCTGCACTTATTTCCTGTGCAAGA 300
QY 479 TCGGATGTAATTAACGGGTATTACTATGTTGGACTACTGGGGCCCAAGGCACCTACGGTC 538
Db 301 GGG-----CATAACTTGTACTACTGGGGCCCAAGGCACCGGTC 339
QY 539 ACCGTCTCCTCAGGTGGAGCGGTTTCAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGAT 598
Db 340 ACCGTCTCCTCAGGTGGAGCGGTTTCAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGAC 399
QY 599 ATCGAGCTCAGTCAGTCTCCATCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACATA 658
Db 400 ATCGAGCTCAGTCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACATA 459
QY 659 TCTCTGCAGAGCCAGTGAAAAGTGTGATAGTATTGGCGATAGTTTATGCACTGGTATCAG 718
Db 460 TCTCTGCAGAGCCAGTGAAAAGTGTGATAGTATTGGCGATAGTTTATGCTGGTACCAG 519
QY 719 CAGAAACAGGACAGCCACCCAAACTCTCATCTATCTGTCATCTGTCATCTAGAACCTTAGAATCTGGA 778
Db 520 CAGAAACAGGACAGCCACCCAAACTCTCATCTATCTTTCGCAACCACTTAGGATCTGGG 579
QY 779 GTCCCTGCCAGGTTCAAGTGGCAGTGGGTCTGAGTCAGACTTCACTCTCACCATCGATCCT 838
Db 580 GTCCCTGCCAGGTTCAATGGCAGTGGGTCTAGGACAAACTTCACTCCTCACCATCGATCCT 639
QY 839 GTGGAGGAAGATGATGCTGCAGTGTATTACTGTCTGCAAAAGTATGGAAGATCCGTACACG 898
Db 640 GTGGGGGCTGATGATGCTGCAACCTATTACTGTGACCAAAATTAATGAGGATCCGTACACG 699
QY 899 TTCCGAGGGGGGACCAAGCTGGAATAAACAAC 929
Db 700 TTCCGAGGGGGGACCAAGCTGGAATAAACAAC 730

RESULT 11
AAZ44206
ID AAZ44206 standard; DNA; 925 BP.
XX
AC AAZ44206;
XX
DT 31-MAR-2000 (first entry)
DE Murine derived DNA fragment #4.
XX
KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KW HIV infection; autoimmune disease; murine; ds.
XX
OS Mus sp.
XX
PN WO9961629-A1.
XX
PD 02-DEC-1999.
XX
PF 24-MAY-1999; 99WO-JP002711.
XX
PR 25-MAY-1998; 98JP-00159957.
XX
PR 26-MAY-1998; 98JP-00161023.
XX
PA (ASAH) ASAH KASEI KOGYO KK.
PA (ASAH) ASAH MEDICAL CO LTD.

XX Ono M, Soka T, Morimoto I, Miyamura K;
 XX WPI: 2000-086720/07.
 XX P-PSDB; AAY51142.
 XX Devices containing antibodies recognising CD4 or CD34 and their use for
 XX the separation of CD4 or CD34 positive cells.
 XX Claim 22; Page 82-84; 11pp; Japanese.
 XX This invention describes a novel device (I) for separating cluster
 XX differentiation (CD)-positive cells using a recombinant (chimeric or
 XX single-chain) antibody recognising CD4 or CD34. The devices are useful
 XX for the separation of CD4 or CD34 positive cells, which is useful for the
 XX collection of hematopoietic undifferentiated cells, elimination of
 XX lymphocytes from cells to be used in bone marrow transplantation, the
 XX detection of leukemic cells and the production of medicinal compositions
 XX for the treatment of HIV infection and autoimmune diseases. This sequence
 XX encodes a murine derived protein fragment which is used to illustrate the
 XX method of the invention
 XX SQ Sequence 925 BP; 223 A; 236 C; 268 G; 198 T; 0 U; 0 Other;
 Query Match 50.7%; Score 522.6; DB 3; Length 925;
 Best Local Similarity 79.3%; Pred. No. 2.3e-121;
 Matches 637; Conservative 0; Mismatches 154; Indels 12; Gaps 1;
 QY 136 GACCACTGCCAAGTTTCGACTCCCGAGCGGCCGACCGCCATGCGCAGGTCAAGCT 195
 DB 18 GACCGCTGCTGGTCTGCTGCTCTCGCGGCCGAGCGGCCATGSCCCAGGTTCAGCT 77
 QY 196 GCAGCAGTCAGCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 255
 DB 78 GCAGCAGTCAGCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 137
 QY 256 TTCTGGCTACACATTCAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 315
 DB 138 TTCTGGCTACACATTCAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 197
 QY 316 TCTAGAGTGGATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 375
 DB 198 CTTGAGTGGATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 257
 QY 376 CAAAGGCAAGGCCCAACTGACTGATGATGATGATGATGATGATGATGATGATGATGAT 435
 DB 258 CAAAGGCAAGGCCCAACTGACTGATGATGATGATGATGATGATGATGATGATGATGAT 317
 QY 436 CAGACTGACATCTGAGGATTTCTGCCATTTATTTATTTGCAAGATCGGATGATTAACGG 495
 DB 318 CAGCCTGACATCTGAGGATTTCTGCCATTTATTTATTTGCAAGATCGGATGATTAACGG 365
 QY 496 GTATTACTATGCTTTGGACTTACTGCGGCCCAAGGACTACCGTCCAGGTCTCTCAGGTGG 555
 DB 366 AACTGGGACGGGTTTGTCTTACTGCGGCCCAAGGACTTCTGCTCAGGTGG 425
 QY 556 AGCGGTTACGGCGAGGTGGCTCTGCGCGTGGCGGATCGATATCGAGTCTACTCAGTC 615
 DB 426 AGCGGTTACGGCGAGGTGGCTCTGCGCGTGGCGGATCGATATCGAGTCTACTCAGTC 485
 QY 616 TCCATCTCTTTGGCTGTCTCTAGGCGAGGCGCCACCATATCTCTGAGAGCCAGTGA 675
 DB 486 TCCATCTCTTTGGCTGTCTCTAGGCGAGGCGCCACCATATCTCTGAGAGCCAGTGA 545
 QY 676 AAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 735
 DB 546 AAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 605
 QY 736 ACCCAACTCTCTATCTGCTGATCCCACTAGAAATCTGAGTCCCTGCGCAGGTTCAG 795
 DB 606 ACCCAACTCTCTATCTGCTGATCCCACTAGAAATCTGAGTCCCTGCGCAGGTTCAG 665
 QY 796 TGSCAGTGGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 855

DB 666 TGGCAGTGGTCTGGGACAGACTTCACTTCAACATCCATCTCTGTGGAGAGGATGC 725
 QY 856 TGCAGTGTATTACTGTCTGCAAGATATGGAAGATCCGTACACGTTCCGAGGGGGACCA 915
 DB 726 TGCAACCTATTACTGTCTGCAAGATATGGAAGATCCGTACACGTTCCGAGGGGGACCA 785
 QY 916 GCTGGAATATAAAGCGGCGCGCG 938
 DB 786 GCTGGAATATAAAGCGGCGCGCG 808
 RESULT 12
 AA258664
 ID AA258664 standard; cDNA to mRNA; 925 BP.
 XX AA258664;
 AC
 DT 17-APR-2000 (first entry)
 XX
 DE Antibody 4H5 L chain encoding nucleotide sequence.
 XX
 KW CD4 antigen; anti-human; antibody; 4H5; drug; ds.
 XX
 OS Mus sp.
 XX
 PN JP11332563-A.
 XX
 PD 07-DEC-1999.
 XX
 PF 26-MAY-1998; 98JP-00163034.
 XX
 PR 26-MAY-1998; 98JP-00163034.
 XX
 PA (ASAH) ASAH KASBI KOGYO KK.
 XX
 DR WPI: 2000-091351/08.
 DR P-PSDB; AAY59265.
 XX
 PT An antibody and the nucleic acid coding the antibody.
 XX
 PS Disclosure; Page 17-18; 25pp; Japanese.
 XX
 CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the antibody 4H5 L chain encoding nucleotide sequence
 XX
 SQ Sequence 925 BP; 223 A; 236 C; 268 G; 198 T; 0 U; 0 Other;
 Query Match 50.7%; Score 522.6; DB 3; Length 925;
 Best Local Similarity 79.3%; Pred. No. 2.3e-121;
 Matches 637; Conservative 0; Mismatches 154; Indels 12; Gaps 1;
 QY 136 GACCACTGCCAAGTTTCGACTCCCGAGCGGCCGACCGCCATGCGCAGGTCAAGCT 195
 DB 18 GACCGCTGCTGGTCTGCTGCTCTCGCGGCCGAGCGGCCATGSCCCAGGTTCAGCT 77
 QY 196 GCAGCAGTCAGCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 255
 DB 78 GCAGCAGTCAGCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 137
 QY 256 TTCTGGCTACACATTCAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 315
 DB 138 TTCTGGCTACACATTCAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 197
 QY 316 TCTAGAGTGGATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 375
 DB 198 CTTGAGTGGATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 257
 QY 376 CAAAGGCAAGGCCCAACTGACTGATGATGATGATGATGATGATGATGATGATGATGAT 435
 DB 258 CAAAGGCAAGGCCCAACTGACTGATGATGATGATGATGATGATGATGATGATGATGAT 317

QY 436 CAGACTGACATCTGAGGATTCGCCATTTATTATTGTGCAAGATCGATGGTAATTACGG 495
 DB 318 CAGCCTGACATCTGAGGACTCTGGGTCTATTCTGTGCAAGA-----CGCG 365
 QY 496 GTATTACTATGCTTTGGACTACTGGGGCCAAAGCACTACGGTCAACGCTCTCTCAGGTGG 555
 DB 366 AACTGGGACGGGGTTTGTCTACTGGGGCCGAGGGACTCTGGTCACTGTCTCTGCAAGTGG 425
 QY 556 AGCGGTTTCAGGCGGAGGTGGCTCTGGCGTGGGGATCGGATATCGAGTCACTCAGTC 615
 DB 426 AGCGGTTTCAGGCGGAGGTGGCTCTGGAGGTGGCGATCGGACATTTGTGTGACCCCAATC 485
 QY 616 TCCATCTCTCTTTGGCTGTCTCTAGGGCAGAGGGCCACCATATCTCTGAGAGCCAGTGA 675
 DB 486 TCCAGCTCTCTTTGGCTGTCTCTAGGGCAGAGGGCCACCATCTCTCTGCAAGGCCA 545
 QY 676 AAGTGTGATAGTATGCGGATAGTTTATGCACTGTATCAGCAAGAAACAGGACAGCC 735
 DB 546 AAGTGTGATAGTATGCGGATAGTTTATGCACTGTATCAGCAAGAAACAGGACAGCC 605
 QY 736 ACCCAACTCTCTATCTGTCATCCCACTAGATCTGGAATCCCTGCCAGGTTTCA 795
 DB 606 ACCCAACTCTCTATCTGTCATCCCACTAGATCTGGAATCCCTGCCAGGTTTCA 665
 QY 796 TGGCAGTGGGTCTGAGTCAGACTTCACTCTCACCATCGATCTCTGGAGGAAGATGATGC 855
 DB 666 TGGCAGTGGGTCTGGACAGACTTCACTCTCACCATCGATCTCTGGAGGAAGATGATGC 725
 QY 856 TGCAGTGTATTACTGTCTGCAAGTATGGAAGATCCGTACACGTTCCGAGGGGGACCAA 915
 DB 726 TGCACACCTATTACTGTCTGACAAAGTAGTGAGGATCTCTCCGACGTTCCGTGGAGGCCAA 785
 QY 916 GCTGGAATAAAGCGGGCGCG 938
 DB 786 GCTGGAATAAAGCGGGCGCG 808

RESULT 13
 ACCT79607
 ID ACC79607 standard; DNA; 1817 BP.
 XX AC ACCT79607;
 XX AC ACCT79607;
 DT 05-AUG-2003 (first entry)
 DE Plasmid pSK2 scFv19-LL-Db3 nucleotide sequence.
 XX Multimeric single chain tandem Fv-antibody; antibacterial; virucide;
 KW cytostatic; cytokine antagonist; diagnosis; viral disease; prion disease;
 KW bacterial disease; tumoral disease; agglutination; red blood cell;
 KW immune system; tumour cell; cytokine; cytotoxic; gene; ds.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH 123..1811
 FT /*tag= a
 FT /product= "Plasmid pSK2 scFv19-LL-Db3 protein"
 FT
 XX BP1293514-A1.
 XX
 XX 19-MAR-2003.
 XX
 XX 14-SEP-2001; 2001EP-00122104.
 XX
 XX 14-SEP-2001; 2001EP-00122104.
 XX
 XX (AFFI-) AFFIMED THERAPEUTICS AG.
 XX
 XX Le Gall F, Kipriyanov S, Reusch U, Moldenhauer G, Little M;
 XX WPI; 2003-395536/38.
 DR

P-PSDB; ABR57059.

New multimeric Fv-antibody having monomers forming antigen-binding units and sites, useful for the preparation of a pharmaceutical composition for the treatment of a viral, bacterial, tumoral or prion diseases.

Example 1; Fig 7A-B; 29pp; English.

The present invention describes a multimeric Fv-antibody (I) comprising: (a) monomers comprising at least 4 variable domains of which two neighbouring domains of one monomer form an antigen-binding VH-VL or VL-VH scFv unit; and/or (b) at least 2 variable domains of a monomer that are non-covalently bound to 2 variable domains of another monomer resulting in the formation of at least 2 additional antigen binding sites to form multimerisation motif. Also described is a process for the preparation of (I) comprising ligating DNA sequences encoding the peptide linkers with the DNA sequences encoding the variable domains such that the peptide linkers connect the variable domains resulting in the formation of a DNA sequence encoding a monomer of the multivalent multimeric Fv-antibody, and expressing the DNA sequences encoding the various monomers in an expression system. (I) has antibacterial, virucide and cytostatic activities, and can be used as a cytokine antagonist. The multimeric Fv-antibody is useful for diagnosis. The antibody can also be used for the preparation of a pharmaceutical composition for the treatment of a viral, bacterial, tumoral or prion disease, the agglutination of red blood cells, linking cytotoxic cells of the immune system to tumour cells, or linking activating cytokines, cytotoxic substances or a protease to a target cell. The present sequence represents the plasmid pSK2 scFv19-LL-Db3 nucleotide sequence, which is used in the exemplification of the present invention

Sequence 1817 BP; 467 A; 457 C; 478 G; 415 T; 0 U; 0 Other;

Query Match 48.9%; Score 503.4; DB 8; Length 1817;
 Best Local Similarity 74.8%; Pred. No. 1.9e-116;
 Matches 662; Conservative 0; Mismatches 211; Indels 12; Gaps 2;
 QY 137 ACCACTGCGCAAGATTTTCGACTGCCCCGAGGGGGCCAGCCGCGCATGGCCGAGGTCAAGCTG 196
 DB 141 ACGGCAGCGCTGGCTTGTCTGCTGGCAGCTCAGCCGCCCATGGCGAGGTGCAACTG 200
 QY 197 CAGCAGTCAGGGGCTGAGCTGGTGAGGCTGGGGTCTCAGTGAAGATTTCCTCAGAGGT 256
 DB 201 CAGCAGTCGGGGCTGAGCTGGTGAGGCTGGGGTCTCAGTGAAGATTTCCTCAGAGGT 260
 QY 257 TCTGGCTCACATTTCACTGATTTATGATGAGTGGGTGAACAGAGTCAATGCAAGAGT 316
 DB 261 TCTGGCTATGCATTCAGTACTGATGATGAGTGGGTGAACAGAGTCAATGCAAGAGT 320
 QY 317 CTAGAGTGGATTGGACTTTATTAGTACTTACTATGTTGATCTCTAGTTTACACAGAGGTT 376
 DB 321 CTTGAGTGGATTGGACAGATTGGCCCTGGAGATGTTGATACTAATACATGGAAGTTTC 380
 QY 377 AAGGCAAGGCCCAATGACTGTAGACAAATCTCCCAACAGACGCTATTTGGAACTTGC 436
 DB 381 AAGGGTAAAGCCCACTCTGACTGCAGACGAATCTCCAGCAGCCCTACATGCAACTCAG 440
 QY 437 AGACTGACATCTGAGGATCTGCACTTTATTATTGTGCAAGATCGGATGTTA-----AT 490
 DB 441 AGCTAGCATCTGAGGACTCTGGGTCTATTCTGTGCAAGCGGAGACTACGACGGTA 500
 QY 491 TACGGGTATTACTATGCTTTGGACTACTGGGGCAAGGCACTACGGTACCGCTCTCTCA 550
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2005, 17:47:52 ; Search time 3356 Seconds

(without alignments)
11682.419 Million cell updates/sec

Title: US-10-089-278-1

Perfect score: 1030

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	336.4	32.7	535	3	AF240170 Mus muscu
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4	333.8	32.4	683	3	AF240172 Mus muscu
5	322.4	31.3	872	7	CK629396 AMO-AA001
6	313.2	30.4	1104	7	CK629846 AM2-AA002
7	311.2	30.2	601	5	BQ474958 carabus49
8	292.6	28.4	1339	7	CK629414 AM1-AA001
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15	277.4	26.9	327	4	BG148320 uu91c06.y
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18	270.2	26.2	823	7	CK632348 AMO-AM000
19	269	26.1	738	4	BG965088 602829160
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21	264.8	25.7	643	6	BY733441 BY733441
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25	257	25.0	831	4	BG966589	BG966589 602834422
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27	251.6	24.4	489	2	BF855922	BF855922 PM2-FN021
28	249.6	24.2	806	4	BI108506	BI108506 602894952
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ALIGNMENTS

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DEFINITION	AF240168					
ACCESSION	AF240168.1	GI:13877288				
VERSION	AF240168.1	GI:13877288				
KEYWORDS	HTC.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	1 (bases 1 to 671)					
AUTHORS	Cui,D.X., Zeng,G.Y., Wang,F., Xu,J.R., Ren,D.Q., Guo,Y.H., Tian,F.R., Yan,X.J., Hou,Y. and Su,C.Z.					
TITLE	Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after gamma-irradiation in mice					
JOURNAL	World J. Gastroenterol. 6 (5), 709-717 (2000)					
PUBMED	11819679					
REFERENCE	2 (bases 1 to 671)					
AUTHORS	Cui,D., Zeng,G., Yan,X., Wang,F., Tian,F., Ren,D., Zhao,T., Li,X. and Su,C.					
TITLE	Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain					
JOURNAL	Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19 (1), 71-80 (2001)					
REFERENCE	3 (bases 1 to 671)					
AUTHORS	Cui,D., Zeng,G., Yan,X., Wang,F., Tian,F., Ren,D., Zhao,T., Li,X. and Su,C.					
TITLE	Direct Submission					
JOURNAL	Submitted (02-MAR-2000) Molecular Cloning Laboratory, Institute of Genetic Diagnosis, Fourth Military Medical University, No. 17 Chang Le West Road, Xi'an 710032, China					
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DB 63   CTTGGAGACAGTCAGGATCTCTGCAAGGCTTCTGGATATACCTTCACAACCTGCTGGA 122
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QY 344  TACTATGGTGATCCTAGTTACAAACACAGAGGTTCAAGGGCAAGGCCACAATGACTGTAGAC 403
DB 183  CACTCTGGAGTGCMAAGTATGCAGAAAGTTCACAGGACGCTTTCCTCTCTTTGGAA 242
QY 404  AATCTCTCAACACAGCCTATTGGGAATTCGCCAGACTGACATCTCAGAGATTCGCGCAT 463
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QY 464  TATTATTGTCAGATCGGATGCTAATTACGGGTATTACTATCTTTGGACTACTGSGGC 523
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DB 411  AGTGGGGATCGGACATCGTGCTCACCCAGTCTCCAGCTTCTTTGGCTGTCTCTAGGG 470
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QY 764  AACCTAGATCTGGATCTCCCTGCGAGGTTCAAGTGGCAGTGGGTCAGTACAGATTCACT 823
DB 591  AAGCAAGGATCCGGGGTCCCTCGAGGTTTACTGCGCAAGTGGGTCCTGGACAGATTTGAG 650
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LOCUS      AF240170      535 bp      mRNA      linear      HTC 30-APR-2001
DEFINITION Mus musculus MRP7 mRNA.
ACCESSION  AF240170
VERSION    AF240170.1  GI:13877291
KEYWORDS   HTC.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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REFERENCE 1 (bases 1 to 535)
AUTHORS   Cui,D.X., Zeng,G.Y., Wang,F., Xu,J.R., Ren,D.Q., Guo,Y.H.,
           Tian,F.R., Yan,X.J., Hou,Y. and Su,C.Z.
TITLE      Mechanism of exogenous nucleic acids and their precursors improving
           the repair of intestinal epithelium after gamma-irradiation in mice
JOURNAL    World J. Gastroenterol. 6 (5), 709-717 (2000)
PUBMED     11819679
REFERENCE 2 (bases 1 to 535)
AUTHORS   Cui,D., Zeng,G., Yan,X., Wang,F., Tian,F., Ren,D., Zhao,T., Li,X.
           and Su,C.
TITLE      Direct Submission
JOURNAL    Submitted (02-MAR-2000) Molecular Cloning Laboratory, Institute of
           Genetic Diagnosis, Fourth Military Medical University, No. 17 Chang
           Le West Road, Xi'an 710032, China
FEATURES   Location/Qualifiers
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Best Local Similarity 87.6%;   Pred. No. 1.2e-83;
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DB 534  GCGGCCCCAGCGGCCATGCGGCCAGGTGAACTGCAGCAGTCAAGGCTGAGGTGGTGG 475
QY 224  CTTGGGGTCTCAGTGAAGATTTCTGCAAGGGTTCTGGCTACACATTCAGTATATGGT 283
DB 474  CTTGGGGTCTCAGTGAAGATTTCTGCAAGGGTTCCGGCTACACATTCAGTATATCT 415
QY 284  ATGAGCTGGGTGAACACAGAGTCATGCAAGAGCTTAGAGTGGATTGGACTTATTAGTACT 343
DB 414  ATGCACTGGCTGAAGATGAATCATGCACAGAGCTTAGAGTGGATTGGAATTATTAGTACT 355
QY 344  TACTATGGTGATCCTAGTTTACACACAGAGGTTCAAGGGCAAGGCCACAATGACTGTAGAC 403
DB 354  TAGCATGGTAAATACAAACTACAAACCAAGAGTTTAAAGGGCAAGGCCACTATGACTGTGAC 295
QY 404  AAATCTCTCAACACAGCCCTATTTTGGAACTTGCAGACTGCACATCTCAGGATTCGCAATT 463
DB 294  AAATCTCTCATTTACAGCCTATATGGAACTTGCAGATTCACATCTGATGATCTGCAATC 235
QY 464  TATTATTGTCAAGATCGGATGGTAATACGGGTATTACGGGTATTACTATGCTTTGGACTACTGGGC 523
DB 234  TATTACTGTGCAAGA--GGGGCTTACTACGGTAGTTTTTTATTACTTTGACTACTGGGC 178
QY 524  CAAGGCACTACGGTCAACGCTCTCTCAGGTGGAGGGGTTTCAGGCGGAGGTGCTCTGGC 583
DB 177  CAAGGACCAACGGTCAACGCTCTCTCAGGTGGAGGGGTTTCAGGCGGAGGTGCTCTGGC 118
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DB 117  GGTGGCGGATCGGA 104
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Best Local Similarity 88.6%; Pred. No. 7.2e-83;
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DB 469 GGCCCAAGGACACCGTCTCCTCAGGTGA-GGGTTTCAGGCGAGTGGCTC 411
QY 580 TGGCGGTGGCGGATCCGATATCAGTCTCAGTCTCCATCTTCTTTGGCTGTCTCT 639
DB 410 TGGCAGTGGCGGATCGGATCGTGTCTCAGTCTCCAGTCTCAGTCTGTCTCT 351
QY 640 AGGCGAGGGCCACCATATCTTCAGAGCCAGTGAAGTGTGTAGTTATGCGCATAG 699
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LOCUS AM0-AA0013-110902-011-H03 AA0013 Apis mellifera cDNA, mRNA
DEFINITION sequence.
ACCESSION CK629396
VERSION CK629396.1 GI:45753871
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SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Apidae; Apis.
1 (bases 1 to 872)
Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
Ramos,R.G.P., Reis,L.P.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espresafico,E.M.,
Espindola,P.S., Peco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
Silva,W.A. Jr.
Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
Unpublished (2004)
Contact: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Departament of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br
This sequence was derived from the FAPESP Genome Program
High quality sequence start: 66
High quality sequence stop: 625.
Location/Qualifiers

FEATURES

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VERSION CK629846.1 GI:45754321
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SOURCE Apis mellifera (honey bee)

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Apidae; Apis.
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Nunes,P.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
Zago,M.A., Soares,A.E., Bitondi,M.G., Espreatico,E.M.,
Espindola,F.S., Paco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
Silva,W.A. Jr.
Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
Unpublished (2004)
Contact: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Department of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catão Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br
This sequence was derived from the FAPESP Genome Program
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QY 552 GTGAGGCGGTTTCAGGCGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAGCTCACTC 611
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QY 612 AGTCTCCATCTCTTTGGTGTCTCTAGGGCAGAGGGCCACCATATCTCTGAGAGCCA 671
Db 309 AGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGGTCCACCATGACCTGCAGTGCCA 250
QY 672 GTGAAGTGTGTAGTATTATGGCGATAGTTTATGCACTGGTATCAGCAGAAACAGGAC 731
Db 249 GCTCAAGTAT-----ACGTTACATATATTGGTATACCAACAGAGCCTGGAT 205
QY 732 AGCCACCCAACTCCATCTATCGTGCATCCCAACCTAGAAATCTGGAGTCCCTGCCAGGT 791
Db 204 CTTCCCCCAGACTCTGATTTATGACACATCCAACTGGCTCTCGAGTCCCTTTTCGCT 145
QY 792 TCAGTGGCAGTGGTCTGAGTCACTCTCACTCCACCATCGATCGATCTGTGGAGGAAGATG 851
Db 144 TCAGTGGCAGTGGTCTGGGACCTCTTATCTCTCAATCAACCCGAATGGAGGCTGAGG 85
QY 852 ATGCTCCAGTGTATTACTGCTCCAAAGTATGGAAGATCGGTACACGTTCCGGAGGGGGA 911
Db 84 ATGCTGCCACTTATTACTGCCAGAGTGGAGTGATTCCGTATCGTACACGTTCCGGAGGGGGA 25
QY 912 CCAAGCTGGAAATAAAACGGGCGG 935
Db 24 CCAAGCTGGAGCTGAAACGGGCGG 1
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RESULT 8
CK629414/c 1339 bp mRNA linear EST 26-MAR-2004
LOCUS AM1-AA0014-041102-021-D05 AA0014 Apis mellifera cDNA, mRNA
DEFINITION sequence.
CK629414
VERSION CK629414.1 GI:45753889
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera
REFERENCE 1 (bases 1 to 1339)
AUTHORS Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
Zago,M.A., Soares,A.E.E., Bitondi,M.G., Espresafico,E.M.,
Espindola,F.S., Paco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
Silva,W.A. Jr.
Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
Unpublished (2004)
Contact: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Department of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br
This sequence was derived from the FAPESP Genome Program
High quality sequence start: 62
High quality sequence stop: 662.
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/organism="Apis mellifera"
/mol_type="mRNA"
/strain="Africanized"
/db_xref="taxon:7460"
/sex="female, worker"
/dev_stage="adult"
/clone_lib="AA0014"
/note="Organ: whole body"
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ORIGIN

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Query Match 28.4%; Score 292.6; DB 7; Length 1339;
Best Local Similarity 69.8%; Pred.No.3.9e-71;
Matches 463; Conservative 0; Mismatches 174; Indels 26; Gaps 4;
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QY 276 ATTATGGTATGAGCTGGGTGAAACAGAGTCTATGCAAAAGAGTCTTAGAGTGGATTGGACT-T 334
Db 723 AGTATGATATAGCTTCGGTGGAGCAGAACCGCTGAAACAGGACCTTGTAGTGGACTGGAATCG 664
QY 335 ATTAGTACTTATCTATGGTGTATCTAGTTACACAGAGAGTTCAGGGCAGGCCACAATG 394
Db 663 ATTTTTCCTGGAGAGGGGAGTACTGAATACAATGAGAAGTTCAAGGGCAGGGCCACACTG 604
QY 395 ACT-GTAGACAATCTCCCAACACAGCCTATTTTGGAACTTGGCAGACTGACATCTCAGGA 453
Db 603 AGTGTGTAGACAAGTCTCCAGCAGACGCTTATGTGGAGCTCATAGGCTGACATCTCAGGA 544
QY 454 TTCTGCAATTTTATTATTTGTGCAAGATCGGATGGTAAATTACGGGTATTTACTATGCTTTTGA 513
Db 543 CTCTGCTGTCTATTTCTGTGCTAGAGGGGACTACTATAGGCGCTA-----CTTTGA 493
QY 514 CTACTGGGCGCCAAAGGCACTACGGTCACTCCCTCCTCAGTGGAGGGGCTTCAGGCGGAGG 573
Db 492 TTGTGGGTCCAAAGGGACCAAGTCCACCGTCTCTCATGTGGAGGGGTTTCAGGCGGAGG 433
QY 574 TGSCCTCTGGCGGTGGCGGATCGGATATCGAGCTCACTCACTCTCCATCTTCTTTGGCTGT 633
Db 432 TGGCTCTGGCGGTGGCGGATCTGACATTTGAGTCACTCCAGTCTCCAGCAATCATGTCTGC 373
QY 634 GTCTCTAGGGCAGAGGGCCACCATATCTTCGAGAGCCAGTGAAGTGTGTATGATTATGG 693
Db 372 ATCTCCAGGGAGAGGGTCAACCATGACCTGCAGTGCAGTCAAGTATATAC----- 323
QY 694 CGATAGTTTATGCACTGGTATCAGCAGAAACAGCAGACGCCAACCAACTCTCATCTA 753
Db 322 -----GTTACATATATTGGTACCAACAGAAAGCTTGATCTCCCCAGAGCTCTTGATTTA 268
QY 754 TCGTGATCAACACTAGAACTTGGAGTCCCTGCAGGTTTCAGTGGCAGTGGGTCTCAGTC 813
Db 267 TGACACATCAACGTGGCTCTGGAGTCCCTTTTCGCTTCAGTGGCAGTGGGTCTGGGAC 208
QY 814 AGACTTCACTCTCACCATCGATCTCTGTGAGGAAGATGATGTGTCAGTGTATTACTGTCT 873
Db 207 CTCTTATTTCTTCACAATCAACCGAATGGAGGCTGAGGATGCTGCCACTTATTACTGCCA 148
QY 874 GCMAAGTATGGAAGATCCGTACACGTTCCGAGGGGGGACCAAGCTGGAATAAAGCGGC 933
Db 147 GGAGTGGAGTGGTTTATCCGTACACGTTCCGAGGGGGGACCAAGCTGGAGCTGAACGGCT 88
QY 934 GGC 936
Db 87 GCC 85
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RESULT 9

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CK629415/c 1419 bp mRNA linear EST 26-MAR-2004
LOCUS AM1-AA0014-041102-021-H09 AA0014 Apis mellifera cDNA, mRNA
DEFINITION sequence.
CK629415
VERSION CK629415.1 GI:45753890
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera
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REFERENCE 1 (bases 1 to 1419)
AUTHORS Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
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448	Qy	448	CGAGATTCTGCCATTTATTATTGTGCAAGATCGAATGGTAAATTACGGGTATTACTATGC	507
344	Db	344	TGAGGACTCTGCTCTATTCTGTCTAGAGGGGACTACTATAGGCGCTA-----	394
508	Qy	508	TTTGGACTACTGGGGCCCAAGCACACTACGGTCACCGTCTCCTCAGGTGAGAGCGGTTTCAGG	567
395	Db	395	CTTTGATCTGTGGGGCCCAAGGGAACACGGTCACCGTCTCCTCATGTGGAGAGCGGTTTCAGG	454
568	Qy	568	CGGAGGTGGCTCTGGCGTGGCGGATCGGATATCGAGCTCACTCAGTCTCCATCTTCTTTT	627
455	Db	455	CGGAGGTGGCTCTGGCGTGGCGGATCTGACATTTAGCTCACTCCAGTCTCCAGCAATCAT	514
628	Qy	628	GGCTGTGTCTCTAGGGCAGAGGGCCACCATATCTTCGACAGCCAGTGAAGTGTGTATAG	687
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688	Qy	688	TTATGGCGATAGTTTTATGCACTGGTATCAGCAGAAACCAAGGACAGCCACCCAACTCCT	747
569	Db	569	-----ACGTTTACATATATTGGTACCAACAGAGCCTGGATCTCTCCCCAGACTCCT	619
748	Qy	748	CATCTATCGTGCATCCAACTAGAAATCTGGAGTCCCTGCCAGGTTTCAGTGGC	799
620	Db	620	GATTTATGACACATCCCAACGTGGCTCTCGAGTCCCATTTTCGTTCTCAGTGGC	671

RESULT	13
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LOCUS	CK633069
DEFINITION	AM3-AP0011-070602-021-A08 AP0011 Apis mellifera cDNA, mRNA
	672 bp mRNA linear EST 26-MAR-2004

Query Match	27.4%	Score 282.4; DB 7; Length 672;
Best Local Similarity	69.5%	Pred. No. 2.4e-68;

Matches	453;	Conservative	0;	Mismatches	171;	Indels	28;	Gaps	4;
Qy	152	TCGACTGCCCGAGCGGCCCGCCAGCGCGCAATGCGCGAGGTCAAGTGCAGCAGTGCAGGG-GC	210						
Db	44	TGGCCTTTACATGCGCGAGCGCGGACAGGGCCCGAGTGAAGCTGCAGCAGTGCAGGGAAC	103						
Qy	211	TGAGCTGGTCAGCGCTGGGGTCTCAGTGAAGATT---CCTGCAAGGGTTCTCGCTACAC	267						
Db	104	AGAAGTGGTAAGCCGTGGGGCTTCAGCTGAAGTTGTCCGTGCAAGGCTTCTGGCTACAT	163						
Qy	268	ATTCACTGATTATGGTATGAGCTGGGTGAAACAGAGTCAATGCAAAAGAGTCTAGAGTGGAT	327						
Db	164	CTTCACAAGTTATGATATAGACTGGGTGAGGCAGACGCCCTGAACAGGACTTCAGTGGAT	223						
Qy	328	TGGACTTATTAGTACTTACTATCGGTGATCTAGTTTACACACAGAGTTCAAGGGCAAGGC	387						
Db	224	TGGATGGATTTTTCCTGGAGAGGGGAGTACTGAATACAAATGAGAAGTTCAAGGGCAGGGC	283						
Qy	388	CACAATGACTGTAGACAAATCCTCCAACACAGCGCTATTTGGAACTTTGCCAGACTGCATC	447						
Db	284	CACACTGAGTGTAGACAAAGTCTCTCCAGCACAGCCTATATGGAGCTCACTAGGCTGACATC	343						
Qy	448	TGAGGATTCGCCATTATTTATTTGTGCAAGATCGGATGGTAATTACGGGTATTACTATGC	507						
Db	344	TGAGGACTCTGCTGTCTATTTCTGTGCTAGAGGGGACTACTATAGGCGCTA-----	394						
Qy	508	TTTGGACTACTGGGCGCCAGGCACTAGGTACCGCTCTCTCAGTGGAGGCGGTTTCAGG	567						
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Qy	628	GGCTGTGTCTCTAGGCGCAGGGCCACCATATCTCTGCAGAGCCAGTGAAGTGTGTATAG	687						
Db	515	GTCTGCATCTCCAGGGGAGGGGTCAACATGACTCGAGTGCAGCTCAAGTAT-----	568						
Qy	688	TTATGGCGATAGTTTTATGCACCTGGTATCAGCAGAAACCCAGGACAGCCACCCAAACTCCT	747						
Db	569	-----ACGTTACATATATTGGTACCAACAGAAGCCTGGATCTCTCCCCAGACTCCT	619						
Qy	748	CATCTATCGTGCATCAACCTAGAATCTGGAGTCCCTGCGCAGGTTCAAGTGGC	799						
Db	620	GATTTATGACATCAACGTTGCTCTCGAGTCCCAATTTGCTTTCAGTGGC	671						

RESULT 14
BI107286

2107286	BI107286	876 bp	mRNA	linear	EST 26-JUN-2001
LOCUS	602894285F1				
DEFINITION	NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5039325 5', 3' UTR sequence.				

ACCESSION	BI107286
VERSION	BI107286.1 GI:14558179

VERSION	210/200.1	Q1.14350175
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
REFERENCE 1 (bases 1 to 876)

1 (Pages 1-10) 876)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

FEATURES	SOURCE
1. Geographical Location: The study area is located in the northern part of the state, covering a total area of 1,200 square kilometers.	State Geographical Information System (GIS) data.
2. Population: The population of the study area is approximately 1.5 million, with a significant portion being rural.	State Census Bureau data.
3. Climate: The climate is semi-arid, with annual rainfall ranging from 400 to 600 millimeters.	State Meteorological Department records.
4. Economy: The primary economic activities are agriculture and mining.	State Department of Economic Development reports.
5. Infrastructure: The infrastructure is developing, with major roads and a growing network of railways.	State Department of Transport and Infrastructure data.
6. Education: The literacy rate is 75%, with a significant improvement in the last decade.	State Education Department data.
7. Healthcare: The healthcare system is improving, with a growing number of hospitals and clinics.	State Health Department data.
8. Environment: The environment is facing challenges due to deforestation and pollution.	State Environment Department reports.
9. Society: The society is diverse, with a mix of ethnic groups and languages.	State Census Bureau data.
10. Politics: The political system is democratic, with regular elections.	State Election Commission data.

ORIGIN

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High quality sequence stop: 823.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="IMAGE:5039325"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match      27.4%; Score 282.2; DB 4; Length 876;
Best Local Similarity 90.1%; Pred. No. 3e-68;
Matches 302; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 605 CTCATCAGTCTCCATCTTTTGGCTGTCTCTAGGCGAGAGGCCACCATATCTCTGC 664
Db 1 CTGACCAATCTCCAGCTTTTGGCTGTCTCTAAGGCGAGAGGCCACCATATCTCTGC 60

QY 665 AGAGCCAGTGAAGTCTTGATGTTATGGCGATGTTTATGCACCTGGTATCAGCAGAA 724
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QY 725 CCAGGACAGCCACCCAACTCTCATCTATCGTGCAATCCAACTAGAACTCTGGAGTCCCT 784
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QY 785 GCAGGTTTCAAGTGGAGTGGTCTGGGACAGACTTCACCTCACCATTGATCTCTGGAG 844
Db 181 GCAGGTTTCAAGTGGAGTGGTCTGGGACAGACTTCACCTCACCATTGATCTCTGGAG 240

QY 845 GAAGATGATCTCAGTGTATTACTCTGCAAGTATGGAAGTACCGTACAGTTCGGA 904
Db 241 GCTGATGATCTCAGTGTATTACTCTGCAAGTATGGAAGTACCGTACAGTTCGGA 300

QY 905 GGGGGACCAAGCTGGAATAAAACGGCGCGC 939
Db 301 TCGGGACCAAGCTGGAATAAAACGGCGCTGATGC 335

RESULT 15
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LOCUS u91c06.y1 Soares mouse NMGB bcell Mus musculus cDNA clone
DEFINITION IMAGE:3383818.5' Similar to SW:KV3H_MOUSE P01660 IG KAPPA CHAIN
V-III REGION PC 3741/TEPC 111. ; mRNA sequence.

ACCESSION BG148320
VERSION BG148320.1 GI:12651742
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 327)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-i@mail.nih.gov
This clone is available royalty-free through LLMNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:108814
Seq primer: -40RP from Gibco.
Location/Qualifiers
1. .327

FEATURES
source
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
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/clone_lib="Soares mouse NMGB bcell"
/note="Organ: germinal B-cell; Vector: p17T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer 15'
TGTACCAATCTGAAGTGGAGCGCGCTGTTTTTTTTTTTTTTTTTTTTT
T 3'; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p17T3 vector.
Library is normalized; constructed by Bento Soares and
M.Fatima Bonaldo."
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ORIGIN

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Query Match      26.9%; Score 277.4; DB 4; Length 327;
Best Local Similarity 90.5%; Pred. No. 5.2e-67;
Matches 296; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 605 CTCATCAGTCTCCATCTTTTGGCTGTCTCTAGGCGAGAGGCCACCATATCTCTGC 664
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QY 665 AGAGCCAGTGAAGTCTTGATGTTATGGCGATGTTTATGCACCTGGTATCAGCAGAA 724
Db 61 AGAGCCAGTGAAGTCTTGATGTTATGGCGATGTTTATGCACCTGGTATCAGCAGAA 120

QY 725 CCAGGACAGCCACCCAACTCTCATCTATCGTGCAATCCAACTAGAACTCTGGAGTCCCT 784
Db 121 CCAGGACAGCCACCCAACTCTCATCTATCGTGCAATCCAACTAGAACTCTGGAGTCCCT 180

QY 785 GCAGGTTTCAAGTGGAGTGGTCTGGGACAGACTTCACCTCACCATTGATCTCTGGAG 844
Db 181 GCAGGTTTCAAGTGGAGTGGTCTGGGACAGACTTCACCTCACCATTGATCTCTGGAG 240

QY 845 GAAGATGATCTCAGTGTATTACTCTGCAAGTATGGAAGTACCGTACAGTTCGGA 904
Db 241 GCTGATGATCTCAGTGTATTACTCTGCAAGTATGGAAGTACCGTACAGTTCGGA 300

QY 905 GGGGGACCAAGCTGGAATAAAACGG 931
Db 301 GGAGGCTCCAAGCTGGAAATCAAAACGG 327
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Search completed: August 24, 2005, 03:30:16
Job time : 3365 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 23, 2005, 20:04:22 ; Search time 222 Seconds
(without alignments)

7591.734 Million cell updates/sec

Title: US-10-089-278-1

Perfect score: 1030

Sequence: 1 tccaccactctgactcaag.....ccagcccgagtcaggattatc 1030

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq*
- 5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	478.6	46.5	717	4	US-09-473-653-5
2	448	43.5	891	2	US-08-894-922A-9
3	444	43.1	807	4	US-09-674-677-4
4	431.8	41.9	797	2	US-08-894-922A-13
5	424.2	41.2	894	4	US-09-486-814A-1
6	423.2	41.1	780	4	US-09-526-738A-3
7	417.8	40.6	771	4	US-09-526-738A-1
8	407.8	39.6	723	4	US-09-581-345-1
9	405.2	39.3	717	2	US-08-553-497A-17
10	403.2	39.1	1176	3	US-09-142-974B-3
11	403	39.1	810	2	US-08-652-507-1
12	402.4	39.1	864	3	US-09-423-439-47
13	401.6	39.0	1135	4	US-09-203-958A-3
14	400.4	38.9	996	4	US-09-742-693-27
15	398.8	38.7	996	2	US-08-894-922A-4
16	397.6	38.6	780	2	US-08-447-402-6
17	397.6	38.6	1010	3	US-09-070-408-1
18	395.2	38.4	717	3	US-09-142-974B-1
19	394.8	38.3	2019	3	US-09-423-439-31
20	394.8	38.3	2025	3	US-09-423-439-37
21	392.6	38.1	714	4	US-09-798-689-22
22	391.6	38.0	831	2	US-08-403-853-17
23	389.8	37.8	749	3	US-08-983-035A-46
24	389.4	37.8	1679	2	US-08-661-052-15
25	389.4	37.8	1679	3	US-09-188-082-15
26	389.4	37.8	1679	3	US-09-364-088-15
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28	389.2	37.8	756	2	US-08-797-689-17	Sequence 17, Appl
29	389.2	37.8	756	4	US-09-984-186-17	Sequence 17, Appl
30	389.2	37.8	1611	3	US-08-983-035A-37	Sequence 37, Appl
31	388	37.7	777	4	US-10-092-246-7	Sequence 7, Appl
32	388	37.7	777	4	US-10-096-246A-7	Sequence 19, Appl
33	385.6	37.4	732	2	US-08-553-497A-19	Sequence 6, Appl
34	384.8	37.4	777	4	US-10-092-246-6	Sequence 6, Appl
35	384.8	37.4	777	4	US-10-096-246A-6	Sequence 25, Appl
36	381.4	37.0	726	2	US-08-553-497A-25	Sequence 5, Appl
37	380.8	36.7	777	4	US-10-092-246-5	Sequence 27, Appl
38	378.4	36.7	777	4	US-10-096-246A-5	Sequence 43, Appl
39	378.4	36.7	726	2	US-08-553-497A-27	Sequence 50, Appl
40	377.6	36.6	843	3	US-09-423-439-43	Sequence 10, Appl
41	377.2	36.6	843	3	US-09-423-439-50	Sequence 4, Appl
42	369	35.8	1998	3	US-08-279-772A-7	
43	368.6	35.8	719	3	US-08-902-486-10	
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ALIGNMENTS

RESULT 1
US-09-473-653-5
; Sequence 5, Application US/09473653
; Patent No. 6703015
; GENERAL INFORMATION:
; APPLICANT: Solomon, Beka
; APPLICANT: Frenkel, Dan
; TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY
; FILE REFERENCE: 00/20785
; CURRENT APPLICATION NUMBER: US/09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 60/152,417
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..7)
; OTHER INFORMATION: scFv 508F construct
US-09-473-653-5

Query Match		46.5%	Score 478.6; DB 4; Length 717;
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Db	2	AGGTCAACTGCAGGAGTCAGGGCTGAGCTGGTGAAGGCTGGGGTCTCAGTGAAGATTT	61
QY	246	CTGCAAGGGTCTGGCTACACATTCACCTGATTTATGGTATGAGCTGGGTGAAGACAGATC	305
Db	62	CCTGCAAGGGTCTGGCTACACATTCACCTGATTTATGGTATGAGCTGGGTGAAGACAGATC	121
QY	306	ATGCAAGAGTCTAGAGTGGATTTAGTACTTACTTACTTACTTACTTACTTACTTACTTACTT	365
Db	122	ATGCAAGAGTCTAGAGTGGATTTAGTACTTACTTACTTACTTACTTACTTACTTACTTACTT	181
QY	366	ACCAGAGTTCAAGGGCAAGGCACAAATGACCTGTAGACAAATCTCCAAACACAGCTATT	425
Db	182	ACCAGAGTTCAAGGGCAAGGCACAAATGACCTGTAGACAAATCTCCAAACACAGCTATT	241
QY	426	TGGAATCTGCCAGACTGACATCTGAGGATTTGCGCATTTATTATTGTCAGAGATCGGATG	485
Db	242	TGGAATCTGCCAGACTGACATCTGAGGATTTGCGCATTTATTATTGTCAGAGAGGGGCTA	301
QY	486	GTAATTACGGGTATTACTATGCTTTGGACTACTTGGGGCCCAAGGCACACTACGGTCACCGTCT	545

Db 302 CTATGTC-----TACTTTGACTACTGGGCGCAAGTGACCAAGTCCACGGTCAACGGTCT 349
Qy 546 CCTCAGGTGGAGCGGTTTCAAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAGC 605
Db 350 CCTCAGGTGGAGCGGTTTCAAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAGC 409
Qy 606 TCACTCAGTCTCCATCTCTTTGGCTGTGTCTCTAGGCGAGAGGGCCACCATATCTCGCA 665
Db 410 TCACTCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCAACCATGACCTGCA 469
Qy 666 GAGCCAGTGAAGTGTGTAGTATGCGGATAGTTTATGCACTGGTATCAGCAGAAAC 725
Db 470 GTGCCAGTCAAGTAT-----AAGTTACATGCACTGGTATCAGCAGAAC 514
Qy 726 CAGGACAGCCCAACTCCTCATCTATCGTGCATCCCACTAGAACTCTGGAGTCCCTG 785
Db 515 CAGGACCTCCCGCCAAAGATGATTTATGACACATCCCAACTGGCTTCTGGAGTCCCTG 574
Qy 786 CAGGTTCAAGTGGCAGTGGTCTGAGTCAGACTTCACTCTCACCATCGATCCTGTGGAG 845
Db 575 CTGCTTCAAGTGGCAGTGGTCTGAGTCTGAGCTTATTTCTCTCAANTCAGCAGCATGGAG 634
Qy 846 AGATGATCTGCACTGTATTACTGTCTCAAGATGGAAGATCCGTACAGTTCGGAG 905
Db 635 CTGAAGATGCTGCCACTTATTACTGCAATCAGCGGAGTAGTTACCCCAATTCAGCTTCGGAG 694
Qy 906 GGGGACCAAGCTGGAATAAA 928
Db 695 GGGGCGCAAGCTGGAATAAA 717

RESULT 2

US-08-894-922A-9
; Sequence 9, Application US/08894922A
; Patent No. 5863765
; GENERAL INFORMATION:
; APPLICANT: BERRY, Mark John
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOGT, Cornelius P.E.
; APPLICANT: WHITEHEAD, Gary Clark
; TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894, 922A
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9504344.4
; FILING DATE: 03-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00468
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul K.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 60113/241261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)-861-3503
; TELEFAX: (202)-822-0944
; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 891 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
US-08-894-922A-9
Query Match 43.5%; Score 448; DB 2; Length 891;
Best Local Similarity 76.2%; Pred. No. 46e-109;
Matches 613; Conservative 0; Mismatches 140; Indels 51; Gaps 3;
Qy 141 CTGCCGAAGTTTCGACTGCCCGAGCGGCCAGCGGCCATGCGCGAGGTCAAGTCTCAGC 200
Db 62 CAGCGCTGGATTGTTTACTCTCGCTGCGCAACCGGCCATGCGCGAGGTCAAGTCTCAGC 121
Qy 201 AGTCAGGGCTCAGCTGGTGGAGCCCTGGGGTCTCAGTGAAGATTTCCTCGAAGGTTCTG 260
Db 122 AGTCTGGGCTGAACCTGGTGAAGCCCTGGGCCCTTCTGTGAAGCTGTCTCTCAAGGCTTCCG 191
Qy 261 GTTACACATTTCACTGATTTATGATGCTGGGTGAACACAGAGTCAATGCAAGAGTCTAG 320
Db 182 ACTACACCTTCAACAGTTATGATGCTGGTGAAGCAGAGGCTTGCACAGGCTTGG 241
Qy 321 AGTGGATTGGACTTATAGTACTTACTATGGTGAATCTAGTTTCAACAGAGGTTCAAG 380
Db 242 AGTGGATTGGAGAGTTAATCTTACCAAGGCTGCTATTATTACATGAGAGTTCAGA 301
Qy 381 GCAAGCCCAATGACTGTAGCAAAATCTCAACACAGCCTATTGGAACTTGCAGAC 440
Db 302 GCAAGGCCACACTGACTGTAGCAAAATCTTCCAGTACAGCCTACATGCAAGTTCAGAGCC 361
Qy 441 TGACATCTCAGGATTTCTGCCATTTATTATGTGAAGATCGGATGTAATTTACGGGTATT 500
Db 362 TGACATCTCAGGACTCTCGGCTCTATTCTGTGCAAGCGGTATGTAATTTACCT 412
Qy 501 ACTATGCTTTGGACTACTGGGGCCAAAGGCACTACCGTCAACCGTCTCTCAGGTGGAGCG 560
Db 413 -----CCTTTGACTACTGGGGCCAAAGGACCAAGGTCACCGTCTCTCTCA----- 456
Qy 561 GTTCAGGCGGAGTGGCTCTGGGGTGGCGGATCGGATATCGAGTCACTCAGTCTCCAT 620
Db 457 -----CGAATGGATATAAAGGGGACATCGAGCTCACCCAGTCTCCAG 496
Qy 621 CTTCTTTGGCTGTCTCTAGGCGAGAGGGCCACCATATCTCTGAGAGCCAGTGAAGTG 680
Db 497 ATTCTTTGGCTGTCTCTAGGCGAGAGGGCCACCATATCTCTGAGAGCCAGTGAAGTG 556
Qy 681 TTGATAGTTATGGCGATAGTTTATGCACTGGTATCAGAGAAACCCAGACAGCCACCCA 740
Db 557 TTGATAGTTATGGCAATAGTTTATGCACTGGTATCAGAGAAACCCAGACAGCCACCCA 616
Qy 741 AACTCCTCATCTATCGTGCATCCACCTAGAACTCTGAGTCCCTGCGAGGTTCAAGTGGCA 800
Db 617 AACTCCTCATCTATCGTGCATCCACCTAGAACTCTGGGATTTCTTCCAGGTTCAAGTGGCA 676
Qy 801 GTGGGTCTCAGTCAGACTTCACTCTCACCATCGATCTGTGGAGGAAGATGATGCTGCAG 860
Db 677 CTGGGTCTAGGACAGACTTCACTTCACTTAACTCTGTGGAGGCTGATGATGTTGCA 736
Qy 861 TGTATTACTGTCTGCAAAAGTATGGAAGATCC-----GTACAGTTTCGAGGGGGGACCA 914
Db 737 CCTATTATTGTCAACAAAGTATGATGATCCGTACATGTACACGTTTCGAGGGGGGACCA 796
Qy 915 AGCTGGAATAAAGCGGGCGCG 938
Db 797 AGCTGAGATCAAAACGGGATCCG 820

RESULT 3

US-09-674-677-4
; Sequence 4, Application US/09674677
; Patent No. 6562622

	Query Match	43.1%	Score 444;	DB 4;	Length 807;
	Best Local Similarity	76.4%;	Pred. No. 5.1e-108;		
	Matches 584;	Conservative 0;	Mismatches 150;	Indels 30;	Gaps 2;
QY	177	CCATGGCCGAGGTCAAGCTGCAGCAGTCAAGGCGCTGAGCTGTAAGGCTCGGGTCTCAG	236		
DB	1	CCATGGCCGATGTGAAGCTTCAGGAATCAAGGCGCTGAGCTGGTAGGCGCCGGGGTCTCAG	60		
QY	237	TGAAGATTTTCCTGCAAGGGTCTGGCTACACATTCAGTGATTCAGTATGCGTATGAGCTGGGGTGA	296		
DB	61	TGAAGATTAACCTGCAAGGGTTCGGCTACACATTCAGTGATTCAGTATGCGTATGAGTGGGGTGA	120		
QY	297	AACAGAGTCATGCAAAAGAGTCTAGAGTGCATTTGGACTTTATAGTACTTTACTATGCTGATC	356		
DB	121	AGCAGAGTCATGCCAAGAGTCTAGAGTGCATTTGGACTTTATAGTAAATTCCTTTGGTAAATA	180		
QY	357	CTATGTTCAACCAAGAGGTTCAAGGGCAGGCCACAATGACTGTAGACAAATCTCTCCAAACA	416		
DB	181	CAAACCTACAAACCAAGAGTTTGAGGCCAAGGCCACAATGACTGTAGACAAATCTCTCCAAACA	240		
QY	417	CAGCCTATTGTGNACTTGCAGACTGCACATCTGAGGATTCGTCCCATTTATTATGTGCAA	476		
DB	241	CAGGCTATTGTGAACCTTGGCAGATTGACATCTGAGGATTCGTCCCATCTATTACTGTGCAA	300		
QY	477	GATCGGATGTAATTAACGGGTATTACTATGCTTTGGACTACTGCGGGCCAAAGGCACATCGG	536		
DB	301	GA-----GTGATCGACTGGTCTCTCGATGCTGCGGGCCAAAGGACCCAGG	345		
QY	537	TCACCGTCTCTCAGGTGGAGCGGTTCAAGCGGAGGTGGCTCTCGCGGTGGCGGATCGG	596		
DB	346	TCACCGTCTCTCAGGTGGAGCGGTTCAAGCGGAGGTGGCTCTCGCGGTGGCGGATCGG	405		
QY	597	ATATCGAGTCACTAGTCTCATCTTTCTTTGGCTGTGTCTCTAGGCGAGAGGGCCACCA	656		
DB	406	ACATTGTGTGACCCAACTCTCCAGCAATCATGTTGCGCATCTCCAGGGGAGAGGTCACCA	465		
QY	657	TATCCTGCGAGCGGTGAAGTGTGATAGTTATGGCGATAGTTTTATGACATCGGTATC	716		
DB	466	TGACCTTGCAGTGCACCTCACGTGT-----CAGGTACGTGCACTGGGTACC	510		
QY	717	AGCAGAAACACGAGACAGCCACCAACTCCTCATCTATCGTGCATCTCCAACTAGAAATCTG	776		
DB	511	AACAGAAGTTCAGGCACCTCCCCCAAAGATGATTTATGACACATCCAAATCGGCTCTG	570		
QY	777	GAGTCCCTGCCAGGTTCACTGGCAGTGGGTCTGAGTCAGACTTCACTCTCACCATCGATC	836		
DB	571	GAGTCCCTGCTCGCTTTCAGTGGCAGTGGGTCTGGGACCTCTCACCTCTCTCACAATCAGCA	630		
QY	837	CTGTGGAGGAAGATGATGCTGCAGTGTATTAATCTGTCTGCAAGTATGGAAGATCCGTACA	896		

	Query Match	41.9%	Score 431.8;	DB 2;	Length 797;
	Best Local Similarity	77.2%;	Pred. No. 8.8e-105;		
	Matches 586;	Conservative	0;	Mismatches 122;	Indels 51; Gaps 3
Qy	186	AGGTCAAGCTGCACAGCTCAGGGGCTGAGCTGGTGAGGCGCTCTCAGTGAAGATT	245		
Db	13	AGGTGCAGCTGCACAGCATCTGGGCTGACCTGGTGAAGCCCTGGGCTTCTGTGAAGCTGT	72		
Qy	246	CCTGCAAGGGTTCTGGCTACACATTCACTGATATTGGTATGAGCTGGGTGAAACAGAGTCT	305		
Db	73	CCTGCAAGGGTTCCGACTACACCTTCAACCTTATTCGATGCACTCTGGGTGAAGCAGAGGC	132		
Qy	306	ATGCAAGAGCTCTAGAGTGGATTCCGACTTATTAGTACTTACTATGGTGATCCTAGTTACA	365		
Db	133	CTGCAAGGCTTGAAGTGATTCGAGAGATTATCTTACCACACGGTCTGCTTATTACA	192		
Qy	366	ACCAGAGGTTCAAGGGCAAGGCCACAATGACTGTAGACAAATCCTTCAACACAGCGCTATT	425		

RESULT 6

US-09-526-738A-3
; Sequence 3, Application US/09526738A
; Patent No. 6630584
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
; APPLICANT: LTD.
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336
; CURRENT APPLICATION NUMBER: US/09/526,738A
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 780
; TYPE: DNA
; ORGANISM: Humanus
US-09-526-738A-3

Query Match 41.1%; Score 423.2; DB 4; Length 780;
Best Local Similarity 74.9%; Pred. No. 1.7e-102;
Matches 571; Conservative 0; Mismatches 158; Indels 33; Gaps 2;

QY	179	ATGCCCGAGCTCAAGCTGCAGCAGCTCAGGGGCTGAGCTGGTGGGCTGAGTCTCAGTG	238
DB	1	ATGCCCGAGCTCAAGCTGCAGCAGCTGAGGGCTGAGTGGCAAACTGGGGCTCAGTG	60
QY	239	AAGATTTCCTGCAAGGTTCTGGCTACACATTCACCTGATTATGGTATGAGCTGGGTGAAA	298
DB	61	AAGATGTCTGCAAGACTTCTGGCTACACCTTTACTAGCTAGTGAATGAACTGGTAAAA	120
QY	299	CAGAGTCATCAAGAGCTAGAGTGGATTGGACTTATAGTACTTACTATGGTATCCT	358
DB	121	CAGAGGCTCGACAGGCTCTGGAATGGATTGGATACATTAATCCTACCTAGTTACT	180
QY	359	AGTTACAAACAGAGGTTCAAGGGCAAGCCACATGACTGTAGCAAACTCCTCAACACA	418
DB	181	AAGTACATCAGAAGTTCAAGGCAAGGCCACATTTGATCGACAAATCCTCAGCAGC	240
QY	419	GCTATTTTGGAACTTGCCAGACTGACATCTGAGGATTTCTGCCATTTATTTATGCAAGA	478
DB	241	GCCTACATGCAACTGAGCAGCCTGACCAATGTGGACTCTGCAGTCTATTATTGTACAA	298
QY	479	TCGGATGGTAAATTACGGGTATTTACTATGCTTTGGACTACTGGGGCCCAAGGCATCGGTC	538
DB	299	-----CTGTTTACTCTTATTTTGGACTACTGGGGCCCAAGGGACACGGTC	342
QY	539	ACCGTCTCTCAGTGGAGCGGTTTCAAGCGGAGGTGGCTCTGGCGTGGCGGATCGGAT	598
DB	343	ACCGTCTCTCAGTGGAGCGGTTTCAAGCGGAGGTGGCTCTGGCGTGGCGGATCGGAC	402
QY	599	ATCGAGCTCACTCAGTCTCCATCTTCTTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCAT	658
DB	403	ATCGAGCTCACTCAGTCTCCAGCAATCATGTCTGTCATCTCCAGGGGAGAGGTCAACATA	462
QY	659	TCCTGACAGCCAGTGAAGTGTGATAGTTATGGCGATAGTTTATGCACTGGTATCAG	718
DB	463	ACCTGAGTGCAGCTCAAGTGT-----AAATTACATGCACTGGTTCCAG	507
QY	719	CAGAAACAGGACAGGCCCAAACTCCTCATCTATGTCATCCCAACCTPAGAATCTGGA	778
DB	508	CAGAGCCAGGCACTTCTCCAACTTGGATTCTTAGCAATCCCAACCTGGCTTCTGGA	567
QY	779	GTCCCTGCCAGGTTTCAAGTGGAGTGGTCTGAGTCAGACTTCACTCTCACCATCGATCCT	838
DB	568	GTCCCTGCTGCTTCAAGTGGCAGTGGATCTGGACCTCTTACTCTCTCAAACTCAGCCGG	627
QY	839	GTGGAGAGATGATGCTGAGTGTATTACTGTCTGCAAAAGTATGGAAGTCCGTACAG	898
DB	628	ATGGAGGCTGAAGTGTGCTGCACTTATTACTGCGAGCAAAAGGAGTAGTTACCCATACAG	687
QY	899	TTCCGAGGGGGACCAAGCTGGAATAAACAAGCGGCGCGCA	940

Db

RESULT 7

US-09-526-738A-1
; Sequence 1, Application US/09526738A
; Patent No. 6630584
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
; APPLICANT: LTD.
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336
; CURRENT APPLICATION NUMBER: US/09/526,738A
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Humanus
US-09-526-738A-1

Query Match 40.6%; Score 417.8; DB 4; Length 771;
Best Local Similarity 74.8%; Pred. No. 4.5e-101;
Matches 565; Conservative 0; Mismatches 157; Indels 33; Gaps 2;

QY	186	AGGTCAAGCTGCAGCAGCTCAGGGGCTGAGCTGGTGGGCTGAGTGGTCTCAGTGAAGATTT	245
DB	2	AGGTCAAACTGCAGCAGCTCTGGGGCTGAACTGGCAAAACCTGGGGCTCAGTGAAGATGT	61
QY	246	CCTGCAAGGTTCTGGCTACACATTCACCTGATTATGGTATGAGCTGGGTGAACAGAGTC	305
DB	62	CCTGCAAGACTTCTGGCTACACCTTTACTAGCTACTGGATGAATGGGTAAACAGAGGC	121
QY	306	ATCAAAAGAGCTTAGAGTGGATTGGACTTATTAGTACTTACTATGGTATCTTAGTTACA	365
DB	122	CTGGACAGGGCTGGAAATGGATTGGATACATTAATCTTACCCTGGTTACTTAAGTACA	181
QY	366	ACCAGAGGTTCAAGGCAAGGCCACAAATGATCTAGACAAATCCTCAACACAGACCTATT	425
DB	182	ATCAGAAGTTCAAGGCAAGGCCACATTTGACTGCAGACAAATCCTCCAGCAGCGCTACA	241
QY	426	TGGAACCTGCCAGACTGACATCTGAGGATCTGCCATTTATTATTGTCAGAGATCGGATG	485
DB	242	TGCAACTGAGCAGCCTGACCAATGTGGACTCTGCACTCTATTATTGTACAA-----	292
QY	486	GTAATTACGGGTATTACTATGCTTTGGACTACTTGGGGCCAAAGGCATCTACGGTCAACGCT	545
DB	293	-----CTGGTTACTCTTATTTTGGACTACTGGGGCCCAAGGCACACGGTCAACGCTCT	343
QY	546	CCTCAGTGGAGCGGTTTCAAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAGC	605
DB	344	CCTCAGTGGAGCGGTTTCAAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAGC	403
QY	606	TCACTCAGTCTCCATCTCTTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATATCTGCA	665
DB	404	TCACTCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCAACCAATACCTGCA	463
QY	666	GAGCCAGTCAAAAGTGTGATGTTATGGCGATAGTTTATGCACTGCTATCACAGAAAC	725
DB	464	GTGCCAGCTCAAGTGT-----AAATTACATGCACTGGTTCCACAGAAAC	508
QY	726	CAGGACAGCACCACAACTCTCATCTATCTGTGCATCCCAACCTAGAACTTGGAGTCCCTG	785
DB	509	CAGGCACTTCTCCAACTCTGGATTCTTAGCACATCCAACTGGCTTCTGGAGTCCCTG	568
QY	786	CCAGGTTTCAAGTGGAGTGGTCTGAGTCTGAGTCTCACTCTCAACCATCGATCTCTGTGAGG	845
DB	569	CTCGCTTCAAGTGGAGTGGATCTGGGACCTCTTACTCTCTCAAACTCAGCCGATGAGG	628
QY	846	ATGATCATCTCGAGTGTATTACTGTCTGCAAGTATGGAAGTCCGTACACGTTCCGAG	905
DB	629	CTGAAGATCTGCCACTTATTACTGCCAGCAAAAGGAGTAGTTACCCATACACGTTCCGAG	688

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: mouse
STRAIN: Balb/c
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: splenocytes
IMMEDIATE SOURCE:
CLONE: 4 B 2
FEATURE:
NAME/KEY: CDS
LOCATION: 1..717
US-08-553-497A-17

Query Match 39.3%; Score 405.2; DB 2; Length 717;
Best Local Similarity 73.6%; Pred. No. 9.7e-98;
Matches 534; Conservative 0; Mismatches 183; Indels 9; Gaps 1;
QY 185 GAGGTCAAGCTGCAGCAGTGCAGGGCTGAGCTGTGTGAGGCTCGGGTCTCAGTGAAGATT 244
DB 1 GAGGTGAAGCTGCAGGAGTCTGGGGAGACTTAGTGAAGCTCGAGGGTCCCTGAAACTC 60
QY 245 TCCTGCAGGGTCTGCTGCTACACATTTCAGTATATGATGAGCTGGGTGAACAGAGT 304
DB 61 TCCTGTGCAGCTCTGGAATTCATTTCAGTAGTATGGCATGTCTTGGGTTCGGCAGACT 120
QY 305 CATGCAAGAGTCTAGAGTGGATTGGACTTATTAGTACTTACTATGATGATCTCTAGTTAC 364
DB 121 CCAGACAAGAGCTGGAGTCTGTGCAACCACTTAGTAGTGGTGGTCTTACATCTACTAT 180
QY 365 AACACAGAGGTTCAAGGCAAGGCAACATCACTGTAGACAAATCCTCCAAACACAGCCTAT 424
DB 181 CCAGACAGTGTGAAGGGCGATTCCACCATCTCCAGACAGCAATGCCAAGACACCTGTAC 240
QY 425 TTGGAACTTCCAGACATGACATCTGAGGATCTGCCATTTATTATTGTGCAAGATCGGAT 484
DB 241 CTGCAAAATGAGCAGTCTGAAGTCTGAGGACACAGCCATGATTACTGTGCAAGA----- 294
QY 485 GGTAATTACGGGTATTACTATGCTTTTGGACTCTGCGGCCCAAGGCACTACGGTCAACGTC 544
DB 295 ---CTTGAACCCGGGACTATGCTTTTGGACTCTGCGGCCCAAGGGACCAAGGTCACCGTC 351
QY 545 TCCTCAGGTGGAGCGGTTTCAGGCGGAGTGGTCTGCGGGTGGCGGATCGGATATCGAG 604
DB 352 TCCTCAGGTGGCGTGGCTCGGGCGGTGGTGGGTGGCGGCGGATCTGACATGAG 411
QY 605 CTCACTCAGTCTCAATCTTTTGGGTGTCTCTAGGGCAGAGGGCCACCATATCTGTC 664
DB 412 CTCACCCAGTCTCAGCTTCTTTGGGTGTCTCTTAGGGCAGAGGGCCACCATATCTGTC 471
QY 665 AGAGCAGTCAAAAGTGTGATAGTATGGCGATGTTTATGCACTGGTATCAGCAGAA 724
DB 472 AAGACAGACCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 531
QY 725 CCAGGACAGCCACCAAACTCTCATCTATCGTGCAATCCCAACCTAGAACTCGGAGTCCCT 784
DB 532 CCAGGACAGCCACCAAACTCTCATCTATGCTCGATCCCAATCTAGAACTCGGAGTCCCT 591
QY 785 GCAGGTTCAAGTGGCAGTGGTCTGAGTCAAGTTCATCTCTCAATCCATTCGATCTCTGGAG 844
DB 592 GCCAGGTTTATGTCAGTGGTCTGGGACAGACTTCAGCCTCAACATCCATCTCTGGAG 651
QY 845 GAAGATGATGCTCAGTGTATTACTGTCTGCAAGTATGGAAGTATCGGTACAGTTCGGA 904
DB 652 GAGGATGATATGCAATGATTTCTGTGACCAAGTAGGAAGTTTCGTGGTCTGGTTCGTT 711
QY 905 GGGGGG 910
DB 712 GGAGGG 717

RESULT 10
US-09-142-974B-3
Sequence 3, Application US/09142974B
Patent No. 6451995
GENERAL INFORMATION:
APPLICANT: Cheung, Nai-Kong V.
APPLICANT: Larson, Steven M.
APPLICANT: Guo, Hong-Fen
APPLICANT: Rivlin, Ken
APPLICANT: Sadelain, Michel
TITLE OF INVENTION: Single Chain FV Constructs of Anti-Ganglioside GD2
FILE OF INVENTION: Antibodies
FILE REFERENCE: MSK.P-013-USNP
CURRENT APPLICATION NUMBER: US/09/142,974B
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: PCT/US97/04427
PRIOR FILING DATE: 1997-03-20
PRIOR APPLICATION NUMBER: 60/013,703
PRIOR FILING DATE: 1996-03-20
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1176
TYPE: DNA
ORGANISM: Murine
FEATURE:
OTHER INFORMATION: 5F11-scFv-streptavidin
NAME/KEY: unsure
LOCATION: (37)
NAME/KEY: unsure
LOCATION: (79)
US-09-142-974B-3

Query Match 39.1%; Score 403.2; DB 3; Length 1176;
Best Local Similarity 73.5%; Pred. No. 4e-97;
Matches 554; Conservative 0; Mismatches 170; Indels 30; Gaps 2;
QY 186 AGGTCAAGCTGCAGCAGTGCAGGGCTGAGCTGTGTGAGGCTCGGGTCTCAGTGAAGATT 245
DB 2 AGGTGAACCTGCAGCAGTGCAGGACCTGAACTGTGAGCTCGGGCTTCAAGTGAAGATAT 61
QY 246 CTGCAAGGGTTCGCTACACATTCACTGATTTATGATGAGCTGGGTGAACACAGAGTC 305
DB 62 CTGCAAGACTCTCGAACAATACTCACTGAATACACCATGACATGCTGGGTGAAGCAGGCC 121
QY 306 ATGCAAGAGTCTAGAGTGGATTGGACTTATTAGTACTTACTATGATCTAGTTTACA 365
DB 122 ATGGAAGAGCCTTGAGTGGATTGGAGGTATTAACTCTAACAATGGTGGTACTAATCTACA 181
QY 366 ACCAGAGGTTCAAGGGCAAGGCCACCAATGACTGTAGACAAATCCTCCAAACACAGCCTATT 425
DB 182 AGCAGAAGTTCAAGGGCAAGGCCACCATGACTGTAGACAAGTCTCCAGCAGACGCTACA 241
QY 426 TGAACCTGCCAGACTGACATCTGAGGATTTCTGCCATTTTATTATTGTGCAAGATCGGATG 485
DB 242 TGGAGCTCCGCGAGCCTGACATCTGAGGATTTCTGAGTCTATTACTGTGCAAGA----- 294
QY 486 GTAAATTACGGGTATTACTATGCTTTGCACTACTGGGGCCCAAGGCACTACGGTCAACGTCCT 545
DB 295 -----GATACTACGGTCCCGTTTGTCTTACTGGGTCCAAAGGACCAAGTCAACGTCCT 346
QY 546 CCTCAGGTGGAGCGGTTTCAGGCGGAGGTGGCTCTGCGGTGGCGGATCCGATATCGAGC 605
DB 347 CCTCAGGTGGAGCGGTTTCAGGCGGAGGTGGCTCTGCGGTGGCGGATCCGATATCGAGC 406
QY 606 TCACTCAGTCTCCATCTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATATCTCTGCA 665
DB 407 TCACTCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCACCATGACCTGCA 466
QY 666 GAGCAGTGAAGTGTGATGATTATGGCGATAGTTTATGCACTGGTATCAGCAGAAC 725

Db 793 ACCAAGCTCGAGATCAAAACGGG 814

RESULT 13

US-09-203-958A-3

Sequence 3, Application US/09203958A

Patent No. 6682928

GENERAL INFORMATION:

APPLICANT: KELER, Tibor

APPLICANT: GOLDSTEIN, Joel

APPLICANT: GRAZIANO, Robert

APPLICANT: DEO, Yashwant M.

TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR

TITLE OF INVENTION: BINDING COMPONENTS

FILE REFERENCE: MXI-099CPA

CURRENT APPLICATION NUMBER: US/09/203,958A

CURRENT FILING DATE: 1998-12-02

PRIOR APPLICATION NUMBER: 60/067232

PRIOR FILING DATE: 1997-12-02

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1135

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic construct

FEATURE:

NAME/KEY: CDS

LOCATION: (74)...(1132)

US-09-203-958A-3

Query Match 39.0%; Score 401.6; DB 4; Length 1135;

Best Local Similarity 71.0%; Pred. No. 1e-96;

Matches 562; Conservative 0; Mismatches 224; Indels 6; Gaps 2;

Qy 146 GAAGTTTCGACTGCCCGAGCGGCCACCGCGGCATCGGCGAGGTCAGGTCGACGAGTCAAGTCGACGAGTCA 205

Db 146 GATGTTCCAGATTATGCTGGGGCCAGCGCGCCAGATCTGAGATCCAGCTGCAGCAGACT 205

Qy 206 GGGGCTGAGCTGGTGAGGCTCGGGTCTCAGTCAAGATTTCCTGCAAGGGTCTGGCTAC 265

Db 206 GSACCTGAGCTGGTGAAGCCTCGGGCTTCAGTGAAGATATCCTGCAAGGGCTTCGGTTAT 265

Qy 266 ACATTCACTGATTATGTTAGCTGAGCTGGGTGAAACAGAGTCATGCCAAAGAGTCTAGAGTGG 325

Db 266 TCATTCACTGACTACATCATATTTTGGTGAAGCAGAGCCATGGGAAGAGCCTTAGTGG 325

Qy 326 ATTTGACTTATTTAGTACTTACTATGTTGATTCCTAGTTTCAACACAGAGTTTCAAGGGCAAG 385

Db 326 ACTGGAATAATAATCCTTACTATGTTAGTACTAGCTACAACTCTGAAGTTCAAGGGCAAG 385

Qy 386 GCCACATGACTGTAGACAAATCCTCCACACAGAGCCTATTTTGGAACTTGGCAGACTGACA 445

Db 386 GCCACATGACTGTAGACAAATCCTCCAGCAGAGCCTACATGAGCTCAACAGTCTTGACA 445

Qy 446 TCTGAGGATTTCTGCCATTATTATTGTGCAAGATCGATGGTAATTACGGGTAT---TAC 502

Db 446 TCTGAGGACTCTGCAGTCTATTACTGTGTAGAGGAGTTTATTACTACGGTAGTAGCTAC 505

Qy 503 TATGCTTTGGACTACTGGGGCCAAAGCACAFTACCGTCAACCGTCTCTCAGGTGAGGCGGT 562

Db 506 GAGGCGTTTCTTACTTGGGGCCAAAGGACTCTGGTCACTGTCTCTGAGGAGGTGGCGGC 565

Qy 563 TCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAGTCTCACTAGTCTCCATCT 622

Db 566 TCCGGAGGAGGTGGCAGCGAGGGGGCGGATCCGATGTTGTGTGATGATGCCAGACTCCCACT 625

Qy 623 TCTTTTGGCTGTGCTCTAGGGCAGAGGGCCACCATATCTCTGACAGAGCCAGTGAAG--T 679

Db 626 ACTTTTGCATATACCATTTGGACAAACAGCCTCTCCATCTCTTTGCAAGTCAAGTCAGACCTC 685

Qy 680 GTTGTAGTTATGGCGATAGTTTTTATTGCACTGGTGTATCAGCAGAAAACAGACAGCACCCC 739

Db 686 TTAGTAGTGTGATGAAAGACATATTTGAATGGTTGTTACAGAGGCCAGGCCAGTCTCCA 745
Qy 740 AAACCTCTCATCTATCGTGCATCCAACTAGAACTCTGGAGTCCCTGCGAGTTTCAGTGGC 799
Db 746 ACGGCTTAATCTATCTGTGTCTAACTGGACTCTGGAGTCCCTGACAGTTTCACTGGC 805
Qy 800 AGTGGGTCTGAGTCAGACAGTCTCACTCTCACCATCGATCCTCTGGAGGAAGATGATGCTGCA 859
Db 806 AGTGGATCAGGACAGATTTTCACTGAAATCAGCAGAGTGGAGCTGAGGATTTGGGA 865
Qy 860 GTGTATTACTGTCTGAAAGATGGAAGATCCGTACACGTTTCGGAGGGGGGACCAAGCTG 919
Db 866 ATTATTATTGCTGGCAAGTGACATTTTCTCAGACGTTCTGGTGGAGGCCACCAAGCTG 925
Qy 920 GAAATRAAACGG 931
Db 926 GAAATCAAACCG 937
RESULT 14
US-09-742-693-27
; Sequence 27, Application US/09742693
; Patent No. 6579842
; GENERAL INFORMATION:
; APPLICANT: HOWELL, Steven
; APPLICANT: LITTLE, Julie C.
; APPLICANT: VAN DER LOGT, Cornelis P.
; APPLICANT: PARRY, Neil J.
; TITLE OF INVENTION: METHOD OF TREATING FABRICS
; FILE REFERENCE: C7536 (V)
; CURRENT APPLICATION NUMBER: US/09/742,693
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: EP99310431.4
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 27
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-742-693-27
Query Match 38.9%; Score 400.4; DB 4; Length 996;
Best Local Similarity 70.4%; Pred. No. 2.1e-96;
Matches 611; Conservative 0; Mismatches 191; Indels 66; Gaps 3;
Qy 137 ACCACTGCCGAAGTTTCGACTGCCCGAGCGGCCCGCCATGGCCGAGGTCAAGCTG 196
Db 58 ACGGACGCCGTGGATTGTTTATTACTCGCTGCCCAACCGGCCATGGCCAGGTGCAGCTG 117
Qy 197 CAGCAGTCAGGGCTGAGCTGGTGAAGCTGGGTCTCAGTGAAGATTCTCTCAAGGCT 256
Db 118 CAGCAGTCGGGCTGAAGCTGGTGAAGCTGGGCTCTCTGAAAGCTGCTCTCAAGGCT 177
Qy 257 TCTGGCTACACATTCACTGATTATGGTATGATGAGTGGGTGAAACAGAGTCAATGCAAGAGT 316
Db 178 TCGACTACACCTTCCAGCTTATGGATGATGCTGGGTGAAGCAGAGGCTGACAGGC 237
Qy 317 CTAGAGTGGATTGGACTTATTAGTACTTACTATGGTGAATCCTAGTTTACCAACAGAGGTTTC 376
Db 238 CTTGAGTGGATTGGAGAGATTAATCCTACCAACGGTCTGTTTATTACATGAGAAGTTC 297
Qy 377 AAGGCNAGGCCCAATGACTGTAGCAAAATCTCCNACACAGCTTATTGGAACTTGGC 436
Db 298 AAGAGCAAGGCCCACTGACTGTAGCAAAATCTTCCAGTACAGCCCTACATGCAAGCTCAGC 357
Qy 437 AGACTGACATCTGAGGATTCCTGCCATTATTATTGTGCAAGATCGGATGGTAAATTACGGG 496
Db 358 AGCTGACATCTGAGGACTCTGGGTCTATTACTGTGCAAGACGGTATGTTACTCTTTT 417

Qy 497 TATTACTATG----- 506
Db 418 GACTACTGGGCCAAGGGACCAACGGTCAACCGTCTCTCATATAAGAGCTATGGAGCTT 477
Qy 507 -----CITTGGACTACTGGGCCAAGGCACCTACGGTCAACCGTCTCTCCTCAGTGGAGGC 559
Db 478 GCATGCAAAATTTATTTCAGAGGAGACAGTCATAATGAAATACCTATTGCCACGGCAGCC 537
Qy 560 GGTTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGA---TCGGATATCGAGCTCACTCAAGTCT 616
Db 538 CTTGGATTGTTATTACTCGTGGCCCAACCGAGGATGGCCGACATCGAGCTCACCCAGTCT 597
Qy 617 CCATCTCTTTGGCTGTCTCTAGGGCAGAGGGCCACCATATCTTCGACAGCCAGTGAA 676
Db 598 CCAGATTTCTTGGCTGTCTCTAGGGCAGAGGGCCACCATATCTCTGCAGAGCCAGTGAA 657
Qy 677 AGTGTGATAGTTATGCGCATAGTTTATGCACTGCTATCAGCAGAAACAGAGCAGCCCA 736
Db 658 AGTGTGATAGTTATGCGCAATAGTTTATGCACTGCTATCAGCAGAAACAGAGCAGCCCA 717
Qy 737 CCAAACTCTCATCTATCGTGCATCCAACTAGAAATCTGGAGTCCCTGCCAGGTTTCAGT 796
Db 718 CCAAACTCTCATCTATCTGTCATCCAACTAGAAATCTGGGATTCCTGCCAGGTTTCAGT 777
Qy 797 GGCAGTGGGTGAGTCAGACTTCACTCTCAACATCGATCCTCTGTGAGGAGAGATGATGCT 856
Db 778 GGCAGTGGGTCTAGGACAGACTTCAACCTTCAACATTAATCTCTGTGAGGAGGCTGATGAT 837
Qy 857 GCAGTGTATTACTCTGCAAAAGTATGGAAGATCC-----GTACACGTTTCGGAGGGGG 910
Db 838 GCAACCTATTATTGTCAAAAGTATGATGATCCGTATACATGTACACGTTTCGGAGGGGG 897
Qy 911 ACCAAGCTGGAATAAAACGGCGGCCG 938
Db 898 ACCAAGCTCGAGATCAACCGGGGATCCG 925
RESULT 15
US-08-894-922A-4
; Sequence 4, Application US/08894922A
; Patent No. 5863765
; GENERAL INFORMATION:
; APPLICANT: BERRY, Mark John
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOGT, Cornelius P.E.
; APPLICANT: WHITELAM, Gary Clark
; TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,922A
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9504344.4
; FILING DATE: 03-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00468
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokullis, Paul K.
; REGISTRATION NUMBER: 16,773

FRAGME

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;/ TITLE OF INVENTION: DIMERIC AND MULTIMERIC ANTIGEN BINDING STRUCTURE
;/ FILE REFERENCE: 03528.0142.PCUI00
;/ CURRENT APPLICATION NUMBER: US/10/489,626
;/ CURRENT FILING DATE: 2004-03-12
;/ NUMBER OF SEQ ID NOS: 33
;/ SOFTWARE: PatentIn version 3.3
;/ SEQ ID NO 4
;/ LENGTH: 1817
;/ TYPE: DNA
;/ ORGANISM: Artificial
;/ FEATURE:
;/ OTHER INFORMATION: Plasmid
US-10-489-626-4

Query Match 49.0%; Score 505; DB 21; Length 1817;
Best Local Similarity 74.3%; Pred. No. 1.3e-140; Indels 12; Gaps 2;
Matches 663; Conservative 0; Mismatches 210;

QY 137 ACCACTGCCGAAGTTTCAGCTGCCGAGCGCCGAGCCGATGCCGAGGTCAAGCTG 196
DB 141 ACGGACGCCGCTGGCTTGCTGCTGGCAGCTCAGCGGCCATGGCGAGGTGCAACTG 200
QY 197 CAGCAGTCAGGGCTGAGCTGTGAGCCCTGGGGTCTCAGTGAAGATTTCCTGCAAGGGT 256
DB 201 CAGCAGTCTGGGCTGAGCTGTGAGCCCTGGGTCTCAGTGAAGATTTCCTGCAAGGCT 260
QY 257 TCTGGCTACACATTCTCACTGATTATGATGTAGCTGGGTGAAACAGAGTCATGCAAGAGT 316
DB 261 TCTGGCTATGCTATGATGCTACTGGATGAATGGGTGAAGCAGAGGCTGGACAGGT 320
QY 317 CTAGAGTGGATTGGACTTATTAGTACTTACTATGTGTCATCTAGTTTACAACACAGAGTTTC 376
DB 321 CTTGAGTGGATTGGACAGATTGGCTTGGAGTGGTGTACTTAATCTAATGGAAGTTTC 380
QY 377 AAGGGCAAGGCCCAATAGACTGTAGACAAATCTCTCAACACAGCCCTATTGGAACCTTGGC 436
DB 381 AAGGGTAAAGCCACTCTGACTGTCAGACGAATCTCTCCAGCACAGCCCTACATGCAACTCAGC 440
QY 437 AGACTGACATCTGAGATTCTGCCATTATTATTATGTGCAAGATCGATGGTA-----AT 490
DB 441 AGCCTAGCATCTGAGGACTCTGGGTCTATTCTGTGCAAGCGGAGACTACGACGGTA 500
QY 491 TAGCGGTATTACTATCTTTTGAAGTACTTGGGGCAAGGCACTACGGTCAACCGTCTCTCA 550
DB 501 GGCGGTATTACTATGCTATGACTTCTGGGTCAAGGAACTCTAGTCAACCGTCTCTCA 560
QY 551 G-----GTGGAGCGGTTCAAGCGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAG 604
DB 561 GCCAAACCAACCCCAAGCTTGAAGAAGGTGAATTTTCAGAGCACGCGTAGATATCTTG 620
QY 605 CTCACCTCAGTCTCCATCTTTTGGCTGTCTCTAGGGCAGAGGGCCACCATATCTCTGC 664
DB 621 CTCACCAAACTCCAGCTTTCTTTGGCTGTCTCTAGGGCAGAGGGCCACCATCTCTCGC 680
QY 665 AGAGCCAGTGAAGTGTGATAGTTATGCGATAGTTTATGCATGCTGATCAGCAGAA 724
DB 681 AAGCCAGCCAAAGTGTGATATGATGATGATGATTTTGAAGTGGTACCAACAGATT 740
QY 725 CCAGGACGCCCAACCACTCTATCTGTCATCTCAACCTCAAGATCTGAGTCCCT 784
DB 741 CCAGGACGCCCAACCACTCTATCATCATCATCATCATCATCATCATCATCATCATCATCAT 800
QY 785 GCCAGGTTTCAAGTGGAGTGGTCTGATCAGACTTCACTCTCAACATCATCTCTGAGAG 844
DB 801 CCCAGGTTTATGAGGAGTGGGTCTGGGACAGACTTCAACCTTCAACATCATCTCTGAGAG 860
QY 845 GAAGATGATGCTGACGTGATTACTCTCTGCAAGTATGGAAGATCGGTACAGTTCGGA 904
DB 861 AAGTGGATGCTGCAACCTATCACTGTCAAGAAAGTACTGAGGATCCGTGGAGTTCTGTT 920
QY 905 GGGGGACCAAGTGGAAATAAAGCGGGCGGCGCATCGGGTCCGGGGCGGTGGTCTTCT 964
DB 921 GGAGGACCAAGCTGGAATCAAAAGCGGCTGATGCTCGCGCCGCTGGTGGTGGTCTCT 980

QY 965 GGTTGGTCTTCTGGTGGTGGTGGTCTTCTGGTGGTGGTGGTCTTCTGGC 1009
DB 981 GCGGCGGTGGTAGCGGTGGTGGCGGCTCCGGTGGTGGTAGC 1025

RESULT 4

US-09-808-037-5
; Sequence 5, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Bilal
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
; FILE REFERENCE: SOLOMON=2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-09-808-037-5

Query Match 46.5%; Score 478.6; DB 9; Length 717;
Best Local Similarity 80.3%; Pred. No. 7.7e-133;
Matches 597; Conservative 0; Mismatches 119; Indels 27; Gaps 2;

QY 186 AGTCAAGCTGCAGCAGTCAAGGGCTGAGCTGGTGAAGGCTCGGGTCTCAGTGAAGATT 245
DB 2 AGTCAAACTGCAGGAGTCAAGGGCTGAGCTGGTGAAGGCTCGGGTCTCAGTGAAGATT 61
QY 246 CTGCAAGGTTCTGGCTACACATTCACATTCATGATTATGATTGAGTGGTGAACAGAGTC 305
DB 62 CTGCAAGGTTCTGGCTACACATTCACATTCATGATTATGATTGAGTGGTGAACAGAGTC 121
QY 306 ATGCAAGAGTCTAGAGTGGATTGGACTTATTAGTACTTACTATGTTGATCTTAGTACA 365
DB 122 ATGCAAGAGTCTAGAGTGGATTGGAGTTATTAGTACTTACTATGTTGATCTTAGTACA 181
QY 366 ACCAGAGTTCAAGGGCAAGGCCACAATGACTGTAGACAAATCTCTCAACACAGCCTATT 425
DB 182 ACCAGAGTTCAAGGGCAAGGCCACAATGACTGTAGACAAATCTCTCAACACAGCCTATA 241
QY 426 TGAAGTCTCCAGACTGACATCTGAGGATTCGCCATTTATTATTGTGAAGATCGGATG 485
DB 242 TGAAGTCTCCAGACTGACATCTGAGGATTCGCCATTTATTATTGTGAAGATCGGATG 301
QY 486 GTAAATTACGGGTATTACTATGCTTTGGACTACTGGGGCCAAAGGCACTACGGTCACCGTCT 545
DB 302 CTATGTCC-----TACTTTGACTACTGGGGCCAAAGTGAACAGGTCAACCGTCT 349
QY 546 CTTCAAGTGGAGCGGTTCAAGCGGAGTGGCTCTGGCGGTGGCGGATCGGATATCGAGC 605
DB 350 CTTCAAGTGGAGCGGTTCAAGCGGAGTGGCTCTGGCGGTGGCGGATCGGATATCGAGC 409
QY 606 TCACCTCAGTCTCCATCTTCTTTGGCTGTCTCTAGGGCAGAGGGCCACCATATCTGCA 665
DB 410 TCACCTCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCAACATGACCTGCA 469
QY 666 GAGCCAGTGAAGTGTGATAGTATTATGGCGATAGTTTATGCACTGGTATCAGCAGAAAC 725

Db 470 GTGCCAGCTCAAGTAT-----AAGTTACATGCACTGGTATCAGCAGAAGC 514
QY 726 CAGGACAGCCACCAACTCCTCATCTATCGTGCATCCCACTAGAACTCTGGAGTCCCTG 785
Db 515 CAGGACCTCCCCCAAGAGATGGATTATGACACATCCCAACTGGCTTCTGGAGTCCCTG 574
QY 786 CAGGTTTCAGTGGCAGTGGGTCTGAGTCAAGCTTCACTCTCCACATCGATCCTGTGGAGG 845
Db 575 CTCGCTTCAGTGGCAGTGGGTCTGGACCTCTTATTTCTCTCAATCAGCAGCATGGAGG 634
QY 846 AAGATGATGCTGCAGTGTATTACTGTCTGCAAGATGGAAGATCCGTACAGTTCGGAG 905
Db 635 CTGAAGATGCTGCCACTTATTACTGCCATCAGCGAGTAGTTACCCATTCACGTTCCGAG 694
QY 906 GGGGACCAAGCTGGAATAAAA 928
Db 695 GGGGGCCCAAGCTGGAATAAAA 717

RESULT 5
US-10-162-889-5
; Sequence 5, Application US/10162889
; Publication No. US20030077252A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Bilal
; TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME
; TITLE OF INVENTION: USEFUL IN DIAGNOSING
; TITLE OF INVENTION: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
; FILE REFERENCE: SOLOMON=2B
; CURRENT APPLICATION NUMBER: US/10/162,889
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US/09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-162-889-5

Query Match 46.5%; Score 478.6; DB 14; Length 717;
Best Local Similarity 80.3%; Pred. No. 7.7e-133;
Matches 597; Conservative 0; Mismatches 119; Indels 27; Gaps 2;
QY 186 AGGTCAAGCTGCAGCAGTCAAGGGCTCAGCTGTGAGGCTGGGTCTCAGTGAAGATT 245
Db 2 AGGTCAAACTGCAGGAGTCAAGGGCTGAGCTGTGAGGCTGGGTCTCAGTGAAGATT 61
QY 246 CTGCAAGGTTCTGGCTACACATTCACTGATTTATGATGAGTGGGTGAACACAGT 305
Db 62 CTGCAAGGTTCTGGCTACACATTCACTGATTTATGATGAGTGGGTGAACACAGT 121
QY 306 ATGCAAGAGCTTAGAGTGGATTGGACTTTATGATGAGTGGGTGATCTAGTTTACA 365
Db 122 ATGCAAGAGCTTAGAGTGGATTGGAGTTATGATGAGTGGGTGATCTAGTTTACA 181
QY 366 ACCAGAGTTCAAGGGCAAGGCCCAATGATCTGTAGCAAACTCTCCAAACAGCCCTATT 425
Db 182 ACCAGAGTTCAAGGGCAAGGCCCAATGATCTGTAGCAAACTCTCCAGCAGCCCTATA 241
QY 426 TGAACCTGTCAGACTCAGACTCTGAGGATTTGCGCATTTTATTTATGTCAGATCGGATG 485
Db 242 TGAACCTGTCAGACTCAGACTCTGAGGATTTGCGCATTTTATTTACTGTGCAAGAGGGGCTA 301

QY 486 GTAATTACGGGTATTACTATGCTTTGGACTACTGGGGCCCAAGGCATACTCGGTACCCGTCT 545
Db 302 CTATGTCC-----TACTTTGACTACTGGGGCCCAAGTGACCAAGGTACCCGTCT 349
QY 546 CTTCAAGTGGAGCGGTTTCAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAGC 605
Db 350 CTTCAAGTGGAGCGGTTTCAGCGGAGTTGGCTCTGGCGGTGGCGGATCGGATATCGAGC 409
QY 606 TCACCTCAGTCTCCATCTCTTTTGGCTGTCTCTTAGGGCAGAGGGCCACATATCTCTGCA 665
Db 410 TCACCTCAGTCTCCAGCAATCATGTCTGCAATCTCCAGGGGAGAGGTCAACATGACCTGCA 469
QY 666 GAGCCAGTGAAGTGTGTATGATGTTATGGCGATGTTTATGCACTGGTATCAGCAGAAAC 725
Db 470 GTGCCAGCTCAAGTAT-----AAGTTACATGCACTGGTATCAGCAGAAGC 514
QY 726 CAGGACAGCCACCAAACTCCTCATCTATCGTGCATCCCACTAGAACTCTGGAGTCCCTG 785
Db 515 CAGGCACCTCCCCCAAGATGGATTATGACACATCCAAACTGGGCTTCTGGAGTCCCTG 574
QY 786 CCAGGTTTCAGTGGCAGTGGGTCTGAGTCAAGCTTCACTCTCACCATCGATCCTGTGGAGG 845
Db 575 CTCGCTTCAGTGGCAGTGGGTCTGGACCTCTTATTTCTCTCAATCAGCAGCATGGAGG 634
QY 846 AAGATGATGCTGCAGTGTATTACTGTCTGCAAGATGGAAGATCCGTACACGTTCCGAG 905
Db 635 CTGAAGATGCTGCCACTTATTACTGCCATCAGCGAGTAGTTACCCATTCACGTTCCGAG 694
QY 906 GGGGACCAAGCTGGAATAAAA 928
Db 695 GGGGGCCCAAGCTGGAATAAAA 717

RESULT 6
US-10-384-788-5
; Sequence 5, Application US/10384788
; Publication No. US20040013647A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: FRENKEL, Dan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A PLAQUE-FORMING DISEASE
; FILE REFERENCE: SOLOMON=2D.2
; CURRENT APPLICATION NUMBER: US/10/384,788
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 60/371,735
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 09/808,037
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/830,954
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 10/162,889
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/152,417
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/IL00/00518
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-384-788-5
Query Match 46.5%; Score 478.6; DB 17; Length 717;
Best Local Similarity 80.3%; Pred. No. 7.7e-133;

Matches	597;	Conservative	0;	Mismatches	119;	Indels	27;	Gaps	2;
Qy	186	AGGTCAAGCTCAGCAGT	CAGGGGCTGAGCTGGT	GAGCCCTGGGGTCTCAGTGAAGATTT	245				
Db	2	AGGTCAAAATCAGAGGT	CAGGGCTGAGCTGGT	GAGSCCTGGGTCTCAGTGAAGATTT	61				
Qy	246	CCTGCAAGGGTCTTGGCT	TACACATTCAGTATAT	TGTTAGCTGGGTGAAACAGAGTC	305				
Db	62	CCTGCAAGGGTCTTGGCT	TACACATTCAGTATAT	TGTTAGCTGGGTGAAAGCAGAGTC	121				
Qy	306	ATGCAAAAGAGCTTAGAGT	TGGACTTATTTAGTACTT	ATCTATGTGGTATCCTAGTTTACA	365				
Db	122	ATGCAAAAGAGCTTAGAGT	TGGAGTTATTAGTACTT	ATCTATGTGGTATGCTAGCTTACA	181				
Qy	366	ACCAAGAGTTCAAGGGCA	AGGCCCAATAGCTGTAG	ACAAATCCTCCAAACAAGCCTATT	425				
Db	182	ACCAAGAGTTCAAGGGCA	AGGCCCAATAGCTGTAG	ACAAATCCTCCAGCACAGCCTATA	241				
Qy	426	TGGAACTTGCAGAGTCA	CTCAGGATCTCGGATTT	CTGCCATTTATTATGTGCAAGTCGGATG	485				
Db	242	TGGAACTTGCAGAGTCA	CTCAGGATCTCGGATTT	CTGCCATTTATTATGTGCAAGAGGGGCTA	301				
Qy	486	GTAATTAACGGGTATT	TACTATCTTTGGACT	TGGGCGCAAGGCACCTACGGTCAACCGTCT	545				
Db	302	CTATGTCC-----	-----TACTTTGACT	ACTGGGCGCAAGTGACACGGTCAACGTCT	349				
Qy	546	CCTCAGGTGAGGCGGT	TCAAGCGGAGGTGGCT	CTGCGGTGGCGGATCGGATTCGAGC	605				
Db	350	CCTCAGGTGAGGCGGT	TCAAGCGGAGGTGGCT	CTGCGGTGGCGGATCGGACATCGAGC	409				
Qy	606	TCACTCAGTCTCCATCT	TTTGGCTGTGTCTTAGGG	CGAGAGGGCCACCATATCTCTGCA	665				
Db	410	TCACTCAGTCTCCAGCA	ATCATGTCTGCATCTCC	AGGGGGAAGGTCAACATGACCTGCA	469				
Qy	666	GAGCCAGTGAAGTGTT	GATAGTTATGGCGAT	AGTTTTATGCACTGGTATCAGCAGAAAC	725				
Db	470	GTGCCAGCTCAAGTAT	-----	-----AGTTACATGCATCTGGTATCAGCAGAAAC	514				
Qy	726	CAGGACAGCCACCAAA	ACTCCTCATCTATCGT	GCATCCAACTAGAAATCTGGAGTCCCTG	785				
Db	515	CAGGACCTCCCCAAA	AGATGGATTTATGAC	ACATCCAAACTGGCTTCTGGAGTCCCTG	574				
Qy	786	CCAGGTTCAGTGGCAGT	GGGCTCTGAGTCAGACT	TCATCTCAACATCGATCTCTGTGGAGG	845				
Db	575	CTCGCTTCAGTGGCAGT	GGGTCTGGGACCTCTT	ATTCTCTCAAAATCAGCAGCATGGAGG	634				
Qy	846	AAGATGATGCTCGAGT	GTATTTACTGTCTGCA	AAAGTATGGAAGATCCCGTACCGTTCGGAG	905				
Db	635	CTGAAGATGCTGCCACT	TTATTCTGCCATCAG	CGGAGTAGTTACCCATTACGTTTCGGAG	694				
Qy	906	GGGGGACCAAGCTG	GAATAAAAA	928					
Db	695	GGGGGACCAAGCTG	GAATAAAAA	717					

RESULT 7

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US/10-618-856-5
; Sequence 5, Application US/10618856
; Publication No. US20040052766A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: FRENKEL, Dan
; TITLE OF INVENTION: IMMUNIZATION AGAINST
; FILE REFERENCE: SOLOMON=2A
; CURRENT APPLICATION NUMBER: US/10/618,856
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/473,653A
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5

```

```

; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-618-856-5

Query Match      46.5%; Score 478.6; DB 18; Length 717;
Best Local Similarity 80.3%; Pred. No. 7.7e-133;
Matches 597; Conservative 0; Mismatches 119; Indels 27; Gaps 2;

Qy 186 AGGTCAAGCTGCAGCAGCTCAGGGGCTCAGCTGTGTAGGCGCTCGGGTCTCAGTGAAGATTT 245
Db 2 AGGTCAAATGCGAGGAGTTCAGGGGCTCAGCTGTGTAGGCGCTCGGGTCTCAGTGAAGATTT 61

Qy 246 CCTGCAAGGGTCTCTGGCTACACATTCATCTGATTTATGGTATGAGCTGGGTGAAACACAGAGTC 305
Db 62 CCTGCAAGGGTCTCTGGCTACACATTCATCTGATTTATGGTATGAGCTGGGTGAAACAGAGTC 121

Qy 306 ATGCAAAAGAGCTAGAGTGGATTGGACTTATTAGTACTTACTATGGTGATCCTAGTTTACA 365
Db 122 ATGCAAAAGAGCTAGAGTGGATTGGAGTTATTAGTACTTACTTACTTGGTGATGCTAGCTACA 181

Qy 366 ACCAGAGGTTCAAGGGCAAGGCCACAATGACTGTAGACAAATCCTCCAAACACAGGCTTATT 425
Db 182 ACCAGAGGTTCAAGGGCAAGGCCACAATGACTGTAGACAAATCCTCCAGCACAGGCTTATA 241

Qy 426 TGGAACTTGCACAGCTGACACTCTGAGGATTTCTGCCATTTATTATCTGCGAAGATCCGATG 485
Db 242 TGGAACTTGCACAGCTGACACTCTGAGGATTTCTGCCATCTTATTACTGTGCAAGAGGGGCTA 301

Qy 486 GTAATTACGGGTATTACTATGCTTTGGACTACTTGGGGCCAAAGGCACCTACGGTCAACCGTCT 545
Db 302 CTATGTCC-----TACTTTGACTACTTGGGGCCAAAGTGACCAAGGTCAACCGTCT 349

Qy 546 CCTCAGGTGAGGGGGTTTCAGGCGGAGGTGGCTCTGTGCGGTGGCGGATCGGATATCGAGC 605
Db 350 CCTCAGGTGAGGGGGTTTCAGGCGGAGGTGGCTCTGTGCGGTGGCGGATCGGATATCGAGC 409

Qy 606 TCACTCAGCTCCACATCTTTTGGCTGTGCTCTAGGGCAGAGGGCCACCATATCCTGCA 665
Db 410 TCACTCAGCTCCAGCAATCATGTCTGCAATCTCCAGGGGGAAGGTCACCATGACCTGCA 469

Qy 666 GAGCCAGTGAAGTGTGTGATAGTTATGGCGATAGTTTTTATGCACTGGTATCAGCAAAAC 725
Db 470 GTGCCAGTCAAGTAT-----AAGTTACATGCACTGGTATCAGCAGAGC 514

Qy 726 CAGGACAGCACCCAAACTCCTCATCTATCGTGCACTCCAACTAGAAATCTGGAGTCCCTG 785
Db 515 CAGGCACTCCCCCAAAAGATGATTTATGACACATCCAAACTGGGCTTCTGGAGTCCCTG 574

Qy 786 CCAGGTTTCAGTGCAGTGGGTCTGAGTCAGACTTCACTCTCACCATCGATCCTGTGGAGG 845
Db 575 CTGCTTTCAGTGCAGTGGGTCTGGGACCTCTTATTCTCTCAAAATCAGCAGCATGGAGG 634

Qy 846 AAGATGATGTCGAGTGTATTACTGTCTGCAAAAGTATGGAAGATCCGATCCGATCCGGAG 905
Db 635 CTGAAGATGTCGCACTTATTACTGCGCATCAGCGGAGTAGTTACCCATTACGTTGGAG 694

Qy 906 GGGGGGCCAAGCTGGAAATAAAA 928
Db 695 GGGGGGCCAAGCTGGAAATAAAA 717

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RESULT 8

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US-10-749-522-5
; Sequence 5, Application US/10749522
; Publication No. US20050089510A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eliat
; TITLE OF INVENTION: AGENTS AND COM

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1. TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN DIAGNOSING AND TREATING

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; TITLE OF INVENTION: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
; FILE REFERENCE: SOLOMON-2B
; CURRENT APPLICATION NUMBER: US/10/749,522
; CURRENT FILING DATE: 2004-01-02
; PRIOR APPLICATION NUMBER: US/09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 717
; ORGANISM: Homo sapiens
; TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-749-522-5

Query Match          46.5%; Score 478.6; DB 21; Length 717;
Best Local Similarity 80.3%; Pred. No. 7.7e-133;
Matches 597; Conservative 0; Mismatches 119; Indels 27; Gaps 2;

QY 186 AGGTCAAGCTGCAGCAGCTCAGGGGCTGAGCTGGTGAGGCGCTGGGCTCAGTGAAGATT 245
Db 2 AGGTCAAACTGCAGGAGTCAAGGGCTGAGCTGGTGAGGCGCTGGGCTCAGTGAAGATT 61

QY 246 CTGCAAGGGTTCTGGCTACACATTCACATGATTATGATGAGCTGGGTGAAACAGAGTC 305
Db 62 CCTGCAAGGGTTCTGGCTACACATTCACATGATTATGATGAGCTGGGTGAAACAGAGTC 121

QY 306 ATGCAAGAGTCTAGAGTGGATTGGACTTATAGTACTTACTATGCTGATCCCTAGTTACA 365
Db 122 ATGCAAGAGTCTAGAGTGGATTGGAGTTATAGTACTTACTATGCTGATCCCTAGTTACA 181

QY 366 ACCAGAGTTCAAGGGCAAGGCCACAAATGACTGTAGACAAATCCTCAACACAGAGCTATT 425
Db 182 ACCAGAGTTCAAGGGCAAGGCCACAAATGACTGTAGACAAATCCTCAACACAGAGCTATA 241

QY 426 TGGAACTTCCAGACTGACATCTGAGGATTCGCGCATTTATTTATTTGCAAGATCGGATG 485
Db 242 TGGAACTTCCAGACTGACATCTGAGGATTCGCGCATTTATTTATTTGCAAGATCGGATG 301

QY 486 GTAAATTACGGGTATTACTATGCTTGGAGTCTGCGGCCAAGGCATACGGTCACCGTCT 545
Db 302 CTATGTCC-----TACTTTGACTTCTGGGGCCAAAGTGACACCGTCACCGTCT 349

QY 546 CCTCAGGTGAGGCGGTTCAAGGGGAGGTGGCTCTGGCGGTGGCGGATCGGATTCGAGC 605
Db 350 CCTCAGGTGAGGCGGTTCAAGGGGAGGTGGCTCTGGCGGTGGCGGATCGGATTCGAGC 409

QY 606 TCACTCAGTCTCCATCTTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATATCTCGCA 665
Db 410 TCACTCAGTCTCCAGCAATCATGTCTGCACTCTCAGGGGGAAGGTCAACCATGACCTGCA 469

QY 666 GAGCCAGTGAAGTTGATGTTATGCGCATAGTTTATGCACTGGTATCAGCAGAAC 725
Db 470 GTGCCAGCTCAAGTAT-----AAGTTACATGCACTGGTATCAGCAGAAC 514

QY 726 CAGGACAGCCACCCAAACTCCTCATCTATCGTCATCCAACTCAGAACTGGAGTCCCTG 785
Db 515 CAGGACCTCCCCAAAGATGGATTATGACACATCCAACTGGCTTCTGGAGTCCCTG 574

QY 786 CAGGTTTCAGTGGAGTGGGTCTGAGTCAGACTTCACTCTCACCATCGATCCCTGTGAGG 845
Db 575 CTGGCTTCAGTGGCAGTGGGTCTGGGACCTCTTATTTCTCTCACAATCAGCAGATCGAGG 634

QY 846 AAGATGATGCTGAGTGTATTTACTGTCTGCAAGATGGAAGATCGGTACACGTTTCGAG 905
Db 635 CTGAAGATGTGCCATTATTTACTGCCATCAGGGAGTAGTTACCCATTCACGTTTCGAG 694
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QY 906 GGGGACCAAGCTGGAAATAAAA 928
Db 695 GGGGGGCCAAGCTGGAAATAAAA 717

RESULT 9
US-11-073-526-5
; Sequence 5, Application US/11073526
; Publication No. US20050152878A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: FRENKEL, Dan
; APPLICANT: HANAN, Eilat
; TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN DIAG
; FILE REFERENCE: SOLOMON-2C
; CURRENT APPLICATION NUMBER: US/11/073,526
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/830,954
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: PCT/IL00/00518
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
; OTHER INFORMATION:
US-11-073-526-5

Query Match          46.5%; Score 478.6; DB 24; Length 717;
Best Local Similarity 80.3%; Pred. No. 7.7e-133;
Matches 597; Conservative 0; Mismatches 119; Indels 27; Gaps 2;

QY 186 AGGTCAAGCTGCAGCAGCTCAGGGGCTGAGCTGGTGAGGCGCTGGGCTCAGTGAAGATT 245
Db 2 AGGTCAAACTGCAGGAGTCAAGGGCTGAGCTGGTGAGGCGCTGGGCTCAGTGAAGATT 61

QY 246 CTGCAAGGGTTCTGGCTACACATTCACATGATTATGATGAGCTGGGTGAAACAGAGTC 305
Db 62 CCTGCAAGGGTTCTGGCTACACATTCACATGATTATGATGAGCTGGGTGAAACAGAGTC 121

QY 306 ATGCAAGAGTCTAGAGTGGATTGGACTTATAGTACTTACTATGCTGATCCCTAGTTACA 365
Db 122 ATGCAAGAGTCTAGAGTGGATTGGAGTTATAGTACTTACTATGCTGATCCCTAGTTACA 181

QY 366 ACCAGAGTTCAAGGGCAAGGCCACAAATGACTGTAGACAAATCCTCAACACAGAGCTATT 425
Db 182 ACCAGAGTTCAAGGGCAAGGCCACAAATGACTGTAGACAAATCCTCAACACAGAGCTATA 241

QY 426 TGGAACTTCCAGACTGACATCTGAGGATTCGCGCATTTATTTATTTGCAAGATCGGATG 485
Db 242 TGGAACTTCCAGACTGACATCTGAGGATTCGCGCATTTATTTATTTGCAAGATCGGATG 301

QY 486 GTAAATTACGGGTATTACTATGCTTGGAGTCTGCGGCCAAGGCATACGGTCACCGTCT 545
Db 302 CTATGTCC-----TACTTTGACTTCTGGGGCCAAAGTGACACCGTCACCGTCT 349

QY 546 CCTCAGGTGAGGCGGTTCAAGGGGAGGTGGCTCTGGCGGTGGCGGATCGGATTCGAGC 605
Db 350 CCTCAGGTGAGGCGGTTCAAGGGGAGGTGGCTCTGGCGGTGGCGGATCGGATTCGAGC 409

QY 606 TCACTCAGTCTCCATCTTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATATCTCGCA 665
Db 410 TCACTCAGTCTCCAGCAATCATGTCTGCACTCTCAGGGGGAAGGTCAACCATGACCTGCA 469

QY 666 GAGCCAGTGAAGTTGATGTTATGCGCATAGTTTATGCACTGGTATCAGCAGAAC 725
Db 470 GTGCCAGCTCAAGTAT-----AAGTTACATGCACTGGTATCAGCAGAAC 514

QY 726 CAGGACAGCCACCCAAACTCCTCATCTATCGTCATCCAACTCAGAACTGGAGTCCCTG 785
Db 515 CAGGACCTCCCCAAAGATGGATTATGACACATCCAACTGGCTTCTGGAGTCCCTG 574

QY 786 CAGGTTTCAGTGGAGTGGGTCTGAGTCAGACTTCACTCTCACCATCGATCCCTGTGAGG 845
Db 575 CTGGCTTCAGTGGCAGTGGGTCTGGGACCTCTTATTTCTCTCACAATCAGCAGATCGAGG 634

QY 846 AAGATGATGCTGAGTGTATTTACTGTCTGCAAGATGGAAGATCGGTACACGTTTCGAG 905
Db 635 CTGAAGATGTGCCATTATTTACTGCCATCAGGGAGTAGTTACCCATTCACGTTTCGAG 694
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[illegible]

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RESULT 10
US-10-491-653-25
; Sequence 25, Application US/10491653
; Publication No. US20050059082A1
; GENERAL INFORMATION:
; APPLICANT: Breitling, Frank
; APPLICANT: Moldenhauer, Gerhard
; APPLICANT: Poustka, Annemarie
; APPLICANT: Kuhlwein, Thorsten
; APPLICANT: Luttgau, Sandra
; TITLE OF INVENTION: Method for Producing Protein Libraries and for Selecting Proteins
; TITLE OF INVENTION: From Said Libraries
; FILE REFERENCE: 4121-162
; CURRENT APPLICATION NUMBER: US/10/491.653
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: EP 01123596.7
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP02/10852
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 151
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 25
; LENGTH: 1906
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-491-653-25

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	Query Match	44.7%;	Score 460.4;	DB 21;	Length 1906;
	Best Local Similarity	77.9%;	Pred. No. 3.2e+127;		
	Matches 592;	Conservative	0;	Mismatches 141;	Indels 27; Gaps 2;
Qy	186	AGTCAAGCTGCAGCACTCAGGGGCTCAGCTGGTGAGGCGCTGGGGTCTCAGTGAAGATTT	245		
Db	921	AAGTTCAAGCTGCAGCACTCTGGGCTGCACTGGTGAGGCGCTGGGGTCTCAGTGAAGATTT	980		
Qy	246	CCTGCAAGGGTTCTGGCTACACATTCACATTAATGGTATGAGCTGGTGGAACAGAGATC	305		
Db	981	CCTGCAAGGGTTCTGGCTACAAATTCATGATATGCTAGCGCATGGGTGAAACAGAGATC	1040		
Qy	306	ATGCAAAAGAGTCTAGAGTGGATTGCGACTATTACTACTTACTATGGTGATCTCTAGTTACA	365		
Db	1041	ATGCAAAAGAGTCTAGAGTGGATTGGAGTTATTAGTACTTACTATGGTGATCTACTTATA	1100		
Qy	366	ACCAGAGTTCAAGGGCAAGGCCCAATAGCTGTAGACAAATCTCTCAACACAGCCTATT	425		
Db	1101	ACCAGAGTTCAAGGGCAAGGCCCAATAGCTGTGCAAAATCTCTCAGACACAGCCTATA	1160		

QY	426	TGGAACCTTGCAGACTGACATCTGAGGATTCTCGCAATTATTTATTTGTCGAAGATCGGATG	485
Db	1161	TGGAACCTTCCAGACTGACATCTGATGATTCTGCCCATCTATTATTGTGC	1209
QY	486	GTAATTACGGGTATTACTATGCTTTTGACACTACCTGGGGCCAAAGGACATACCGTCAACCGTCT	545
Db	1210	-----CCTGTTACGCCCTTTTGCTTTACTTGGGGCCAAAGGACCAACCGTCAACCGTCT	1259
QY	546	CCTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAGC	605
Db	1260	CCTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAGC	1319
QY	606	TCACCTAGTCTCCATCTTTCTTTTGGCTGTGTCTCTAGGCGAGAGGGCCACCATATCTGTGCA	665
Db	1320	TCACCTAGTCTCCATCTCTCCCTGAGTGTGTCTCAGCAGGAGAGAAAGGTCACTATGAGTGTCA	1379
QY	666	GAGCCAGTGAAGTGTGTGATAGTTATGGCCATAGTTTTA-----TGCACCTGGTATCAGC	719
Db	1380	AGTCCAGTCAAGTCTGTTTAAACAGTGGAAATCAAAATAACAGACTTGGCCCTGGTACCAGC	1439
QY	720	AGAAACAGGACGACGCCACCCAAACTCCTCATCTATCTGTGCATCCAACTAGAAATCTGGAG	779
Db	1440	AGAAACAGGACGACGCTTAAACTGTTGATCTACGGGGCATCCACTAGGGAATCTGGGG	1499
QY	780	TCCCTGCCAGGTTTCAGTGGGAGTGGGTCTGAGTCAAGACTTCACTCTCACCATCGATCCTG	839
Db	1500	TCCCTGATCGCTTTACAGGGCAGTGGATCTCGAAACCGATTTTCACTCTTACCATCAGCAGT	1559
QY	840	TGGAGGAAGATGATGCTGCACTGATTACTGTCTGCAAAAGTATGGAAGATCCCGTACACGT	899
Db	1560	TGCAGGCTGAAGACCTGGCAGTTTATCTGTCAGAAATGATCATAGTTATCCGTTAACGT	1619
QY	900	TCGGAGGGGGGACCAAGCTGGAATAAAACGGCGGCCCGC	939
Db	1620	TCGGTCTGGCACCAGCTGGAATCAAAACGGCGGCCCGC	1659
RESULT 11			
US-10-169-351-68			
; Sequence 68, Application US/10169351			
; Publication No. US20030157090A1			
; GENERAL INFORMATION:			
; APPLICANT: BENVENUTO, EUGENIO			
; APPLICANT: FRANCONI, ROSELLA			
; APPLICANT: DESIDERIO, ANGIOLA			
; APPLICANT: TAVLADORAKI, PARASKEVI			
; TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES			
; TITLE OF INVENTION: WHICH INCLUDE THEM			
; FILE REFERENCE: 4161-4			
; CURRENT APPLICATION NUMBER: US/10/169,351			
; CURRENT FILING DATE: 2002-10-29			
; PRIOR APPLICATION NUMBER: PCT/IT00/00554			
; PRIOR FILING DATE: 2000-12-29			
; PRIOR APPLICATION NUMBER: IT RM99A000803			
; PRIOR FILING DATE: 1999-12-30			
; NUMBER OF SEQ ID NOS: 118			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 68			
; LENGTH: 756			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic			
; OTHER INFORMATION: nucleotide sequence			
US-10-169-351-68			

Query Match	44.68;	Score 459.8;	DB 16;	Length 756;
Best Local Similarity	76.7%;	Pred. No. 3.4e-127;		
Matches 579;	Conservative 0;	Mismatches 167;	Indels 9;	Gaps 1;
Qy	186	AGGTCAAGCTGCGACAGCTCAGGGGCTGAGCTGTGTGAGCGCTGGGGCTTCAGTGAAGATTT	245	
Db	2	AGGTGACAGCTGCGAGAGTCTTGGGGGAGACTTGTAGTCAGCGCTGGAGGCTCCCTGAAACTCT	61	

QY 246 CTTGCAAGGTTCTGGCTACACATTCATGATTTATGTTAGTGGTGGTGAACAGAGTC 305
DB 62 CTTGTCAGGCTCTGGATTCATTTTCAGTAGCTATGGCATGTCTTGGTTCCGACAGTC 121
QY 306 ATGCAAGAGCTTAGAGTGGATTTAGTACTTACTATGTTAGTGTATCTTAGTTACA 365
DB 122 CAGACAAGAGGCTGGAGTTGGTGCACCACTTAATAGTAATGTGGTAGCACCCTTTATC 181
QY 366 ACCAGAGGTTCAAGGCAAGGCCACACATCTAGACAAATCCTCCACAGACCTATT 425
DB 182 CAGACAGTGTGAAGGCGCGATTCAACCATCTCCAGAGACAATGCCAAGAACCCCTGTACC 241
QY 426 TGGAACTTGGCAGACTGCATCTGAGGATTTCTGCCATTTATTATTGTGCAAGATCGGATG 485
DB 242 TGCBAATGACAGCTCTGAAGTCTGAGGACACAGCCATGTATTACTGTGCAAGAAAGGA 301
QY 486 GTAATTACGGGTATTACTATGCT-----TTGGACTACTCGGGCAAGGCACTACGG 536
DB 302 ATTACCCCTATTACTACGGTAGTAGAGGCTACTTTGACTACTGGGCGCAAGGGACCAAG 361
QY 537 TCACCGTCTCCTCAGGTGGAGGCGGTTTCAGGCGGAGTGGCTCTGGGCGTGGCGGATCGG 596
DB 362 TCACCGTCTCCTCAGGTGGAGGCGGTTTCAGGCGGAGTGGCTCTGGGCGTGGCGGATCGG 421
QY 597 ATATCGAGCTCACTCACTCTCCATCTTTCTTTGGCTGTCTCTAGGCGAGAGGCCACCA 656
DB 422 ACATCGAGCTCACTCACTCTCCAGTCTTTTGGCTGTCTCTAGGCGAGAGGCCACCA 481
QY 657 TATCTGCGAGAGCGAGTGAAGTGTGTATGTTATGGCGATGTTTATGCACTGGTATC 716
DB 482 TATCTGCGAGAGCGAGTGAAGTGTGTATGTTATGGCAATAGTTTATGCACTGGTACC 541
QY 717 AGCAGAAACAGGACGACGCCACCACTCTCATCTATCGTGATCCAACTAGATCTG 776
DB 542 AGCAGAAACAGGACGACGCCACCACTCTCATCTATCGTGATTAATCTAGATCTG 601
QY 777 GAGTCCCTGCGAGGTTCACTGGCAGTGGGTCTGAGTCAGACTTCACTCTCACCATCGATC 836
DB 602 GGATCCCTGCGAGTTCAGTGGCAGTGGGTCTAGGACAGACTTCACTCACCATTAAATC 661
QY 837 CTGTGAGGAAGATGATGCTGCGAGTGTATTACTGTCTGCAAGATATGGAAGATCCGTACA 896
DB 662 CTGTGAGGCTGATGATGTTGCAACCTATTACTGTGCAAGAAAGTAATAGGATCCGTGGA 721
QY 897 CGTTCCGAGGGGAGCAACAGCTGGAATAAAGCG 931
DB 722 CGTTCCGAGGGAGCAACAGCTCGAGATCAAGCG 756

RESULT 12
US-10-489-626-6
; Sequence 6, Application US/10489626
; Publication No. US20050079170A1
; GENERAL INFORMATION:
; APPLICANT: LEGALL, Fabrice
; APPLICANT: KIPRIYANOV, Sergey
; APPLICANT: REUSCH, Uwe
; APPLICANT: MOLDENHAUER, Gerhard
; APPLICANT: LITTLE, Melvyn
; TITLE OF INVENTION: DIMERIC AND MULTIMERIC ANTIGEN BINDING STRUCTURE
; FILE REFERENCE: 03528.0142.PCUS00
; CURRENT APPLICATION NUMBER: US/10/489, 626
; CURRENT FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 1817
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Plasmid
US-10-489-626-6

Query Match 43.4%; Score 447; DB 21; Length 1817;
Best Local Similarity 75.7%; Pred. No. 3.3e-123;
Matches 590; Conservative 0; Mismatches 165; Indels 24; Gaps 2;
QY 184 CGAGGTCACAGCTGACAGCTCAGGGGCTGAGCTGTGAGGCTTCTCAGTGAAGAT 243
DB 995 CCAGGTGCAGCTGACAGAGTCTGGGCTGAGCTGTGAGGCTTCTCAGTGAAGAT 1054
QY 244 TTCTCTCAAGGTTCTGGCTACACATTCATGATTATGTTAGTGGTGAAGACAGAG 303
DB 1055 TTCTCTCAAGGTTCTGGCTATGCAITTCAGTAGCTACTGATGAACTGGGTGAAGCAGAG 1114
QY 304 TCATGCAAAAGAGTCTAGAGTGGATTTCGACTTATTTAGTACTTACTTGTGATCTTAGTTA 363
DB 1115 GCCTGCAAGGTTCTTGTAGTGGATTTCGACAGATTTGGCCCTGGAGATGGTGATACTA 1174
QY 364 CAACAGAGGTTCAAGGGCAAGGCCACAATGACTGTAGACAAATCTCCACACAGCCTA 423
DB 1175 CAATGAAAGTTCAAGGGTAAAGCCACTCTGACTGCAGACGAATCTCCAGCACAGCCTA 1234
QY 424 TTTGGAACTTGCAGACTGACATCTCAGGATTTCTGCCATTTATTATTGTGCAAGATCGGA 483
DB 1235 CATGCAACTCAGCAGCTAGCATCTCAGGACTCTCGCGTCTATTTCTGTGCAAGACGGGA 1294
QY 484 TGGTA-----ATTACGGGTATTACTATCTTTGGACTACTTGGGCGCAAGGCACTACGGT 537
DB 1295 GACTACAGCGTAGGCGGTTATTACTATGCTATGGACTACTGGGCTCAAGGAACCTCAGT 1354
QY 538 CACCGTCTCCTCAGGTGGAGGCGGTTTCAGGCGGAGTGGCTCTGGGCGTGGCGGATCGGA 597
DB 1355 CACCGTCTCCTCAGCGCAAAACCAACCCCAAGCTTTGGCGG-----TGA 1396
QY 598 TATCGAGCTCACTCAGTCTCCATCTTTTGGCTGTGTCTTAGGCGAGAGGCCACCAT 657
DB 1397 TATCTTGTCAACCAAACTCCAGCTTCTTTGGCTGTGTCTTAGGCGAGAGGCCACCAT 1456
QY 658 ATCTCTGCAGAGCAGTGAAAGTGTGATAGTTATGGCGATAGTTTATGCACCTGGTATCA 717
DB 1457 CTCTCTCAAGGCCAGCCAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1516
QY 718 GCAGAAACAGGACAGCAGCCCAAACTCCTCATCTATCGTGATCCCAACCTAGAACTGG 777
DB 1517 ACAGATTCCAGGACAGCAGCCCAAACTCCTCATCTATGATGCAATCCAATCTAGTTCTGG 1576
QY 778 AGTCCCTGCCAGTTCAGTGGCAGTGGGTCTGAGTCAGACTTCACTCTCACCATCGATCC 837
DB 1577 GATCCCAACCGAGTTTAGTGGAGTGGGTCTGGGACAGACTTCACCTCAACATCCATCC 1636
QY 838 TGTGAGGAAGATGATGCTGCAAGTGTATTATCTGTCTGCAAGATGATGGAAGATCCGTACAC 897
DB 1637 TGTGGAGAAGTGGATGCTGCAACCTATCACTGTGCAAGAAAGTACTGACGATCCGTGGAC 1696
QY 898 GTTCGAGGGGGAGCCCAAGCTGGAATAAAGCGGGCGGCGATCGGGTCCCGGGGGCGG 956
DB 1697 GTTCGGTGGAGGCCCAAGCTGGAATAAAGCGGGCTGATGCTTCGGCCCGCTGGATCCG 1755

RESULT 13
US-10-408-930-4
; Sequence 4, Application US/10408930
; Publication No. US20030170820A1
; GENERAL INFORMATION:
; APPLICANT: Coia, et al.
; TITLE OF INVENTION: CONTINUOUS IN-VITRO EVOLUTION
; FILE REFERENCE: 674537-2003.1
; CURRENT APPLICATION NUMBER: US/10/408, 930
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: PCT/AU99/00341
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 09/674,677
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: AU PP3445

; PRIOR FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Homo Sapeins
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(807)
; OTHER INFORMATION: Sequence of the anti-hepatitis surface antigen (4C2) scFv
US-10-408-930-4

Query Match 43.1%; Score 444; DB 16; Length 807;
Best Local Similarity 76.4%; Pred. No. 1.9e-122; Indels 30; Gaps 2;
Matches 584; Conservative 0; Mismatches 150;
QY 177 CCATGCGCGAGGTCAGCTCCAGAGTCAGGGCTGAGCTGGTGAGGCTTGGGCTCTCAG 236
Db 1 CCATGCGCGAGTGTGAGCTTCAGAGTCAGGGCTGAGCTGGTGAGGCTTGGGCTCTCAG 60
QY 237 TGAAGATTCTCTCAAGGGTTCGGCTACACATTCAGTATGATGATGAGCTGGGTGA 296
Db 61 TGAAGATTACCTCAAGGGTTCGGCTACACATTCAGTATGATGATGATGAGTGA 120
QY 297 AACAGAGTCATCAAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAG 356
Db 121 AGCAGAGTCATCAAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAG 180
QY 357 CTAGTTACCAACAGAGGTTCAAGGGCAAGGCGCAATGAGCTGAGACAAATCTCCAAACA 416
Db 181 CAACACTAACACAGAGTTTGAAGCCAGGCGCAATGAGCTGAGACAAATCTCCAAACA 240
QY 417 CAGCCTATTTGGAACTTCGAGACTGACATCTGAGGATTCGCAATTTATTTGTCAA 476
Db 241 CAGCCTATTTGGAACTTCGAGACTGACATCTGAGGATTCGCAATTTATTTGTCAA 300
QY 477 GATCGGATGTAATTACGGGTATTACTATGCTTTGGACTACTGGGCGCAAGGCACTACGG 536
Db 301 GA-----GTGATCGACTGGTCTTCGATGTCCTGGGCGCAAGGCAACACCGG 345
QY 537 TCACCGTCTCTCAGGTGAGGCGGTTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGG 596
Db 346 TCACCGTCTCTCAGGTGAGGCGGTTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGG 405
QY 597 ATATCGAGCTCATCTAGTCTCCATCTTCTTTTGGCTGTGCTCTAGGCGAGGCGCACCA 656
Db 406 ACATTGTGCTGACCCAACTCTCCAGCAATCATGTTGCGCATCTCCAGGGGAGAGGTCACCA 465
QY 657 TATCCTGCGAGAGTCAGTGAAGTGTGATAGTTATGCGGATAGTTTATGCACTGGTATC 716
Db 466 TGACCTGCGAGTGCACCTACGTT-----CAGGTACGTGCACTGGTACC 510
QY 717 AGCAGAAACAGGACGACCAACCAAACTCTCATCTATCTGTCATCCAACTAGAAATCTG 776
Db 511 AACAGAGTCAGGACCTCTCCCAAAAGATGGATTATGACATCCAACTGCTGCTG 570
QY 777 GAGTCCCTGCGAGGTCAGTGGGAGTGGTCTGAGTCAGACTTCACTCTCACCATCGATC 836
Db 571 GAGTCCCTGCTGCTTTCAGTGGCAGTGGGTCTGGGACCTCTCACTCTCTCACAATCAGCA 630
QY 837 CTGTGAGGAGATGATGCTGAGTGTATTTACTGTCTGCAAGATGGAAGATCCGTACA 896
Db 631 GCTTGGAGGCTGAAGATGCTGCCACTTATTTACTTGCCAGCACTGGAGTAGTAACCTCCCA 690
QY 897 CGTTTCGAGGGGAGCAACAGCTGGAATAAAGCGGCGCGCA 940
Db 691 CGTTTCGAGGCTGAGCAACAGCTGGAATAAAGCGGCGCGCA 734

RESULT 14

US-10-013-173-36

; Sequence 36, Application US/10013173

; Publication No. US20030095977A1
; GENERAL INFORMATION: Stephen C.
; APPLICANT: Goshorn, Scott Stoll
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yunkang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, Jonh M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C1
; CURRENT APPLICATION NUMBER: US/10/013,173
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T84.66 single chain antibody-genomic Streptavidin
; OTHER INFORMATION: fusion construct
US-10-013-173-36

Query Match 42.7%; Score 439.4; DB 14; Length 783;
Best Local Similarity 76.3%; Pred. No. 4.6e-121; Indels 45; Gaps 3;
Matches 599; Conservative 0; Mismatches 141;
QY 185 GAGGTCAAGCTGCGAGCAGTCAGGGGCTGAGCTGGTGAGGCTTGGGCTTCCAGTGAAGATT 244
Db 1 GAGGTTCAGCTGCGAGCAGTCGCGGGCAGAGCTTGTGGAGCCAGGGCTTCCAGTGAAGTTG 60
QY 245 TCTGCAAGGGTCTGGCTACACATTCATGATATTGATGATGAGTGGGTGGAACAGAGT 304
Db 61 TCTGCAAGGGTCTGGCTTCAACATTAAGACACCTATATGCACTGGGTGGAACAGAGG 120
QY 305 CATGCAAGAGCTAGAGTGGATTGACTTATTAGTACTTACTATGCTGATCTTAGTTAC 364
Db 121 CTGCAAGGGCTGGAATGGATTGGAAGATTGATCTCGGAATGGTATAGTAATAT 180
QY 365 AACAGAGGTTCAAGGGCAAGGCCAATGACTGTAGACAAATCTCCCAACACAGCCTAT 424
Db 181 GTCCCGAAGTTCAGGGCAAGGCCAATATAACAGCAGACACATCTCCCAACACAGCCTAC 240
QY 425 TTGGAATCTGCGAGCTGACATCTGAGGATCTGCGCAATTTATTTGTCGAAGATCGGAT 484
Db 241 CTGCACTCACCAGCCTGACATCTGAGGACACTGCGGTCTATTATTGTGTC---TCGGTTT 297
QY 485 GGTAAATTACGGGTATTACTATGCTTTGGACTACTGGGGCCAGGCACTACGGTCACCGTC 544
Db 298 GGTACTACGTGTCTGACTATGCTATGGCTTACTGGGGTCAAGGAACCTCAGTCACCGTC 357
QY 545 TCCTCA-----GGTGGAGCGGTTCA 565
Db 358 TCCTCAAGATCTCTGGTGGCGGTGGCTCGGGCGGTGGGTGGCGGGCTCG 417
QY 566 GCGGAGGTGGCTCTGGCGGTGGCGGATCG---GATATCGAGTCACTCATGCTCTCATCT 622
Db 418 GGTGGTGGTGGGTGGCGGTGGCGGTGGCGGATCTGAGCGACATTTGTGTGCCCAATCTCCAGCT 477
QY 623 TCTTTGGCTGTCTCTAGGCGAGGGCCACCATATCTGCGAGAGCCAGTGAAGTTT 682
Db 478 TCTTTGGCTGTCTCTTGGCGAGGGGCCACTATCTCTGCGAGAGCGGTGAAGTTT 537
QY 683 GATAGTTATGGCGATAGTTTATTTATGCACTGGTATCAGCAGAAACAGGACAGCCACCCAAA 742
Db 538 GATATTTTGGCGTTGGGTTTTTGGCACTGCTGACAGAGAACAGGACAGCCACCCAAA 597
QY 743 CTCCTCATCTATCGTGCATCCAACTCTAGAAATCTGGAGTCCCTGCCAGGTTTCACTGGAGT 802
Db 598 CTCCTCATCTATCGTGCATCCAACTCTAGAAATCTGGAGTCCCTGTCAAGTTTCACTGGCACT 657
QY 803 GGGTCTGAGTCAGACTTCACTCTCACCATCGATCTCTGCGAGGAAGATGATGCTGCAGTG 862

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OM protein - protein search, using sw model

Run on: August 23, 2005, 11:17:23 ; Search time 1533 Seconds
(without alignments)
83.003 Million cell updates/sec

Title: US-10-089-278-6
Perfect score: 1725
Sequence: 1 MDCLTLNLSAEGKVDQASKI.....GSGGGSGGGSGASPVQFI 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1725	100.0	329	4 AAB70840	Aab70840 SNV-env 1
2	1239	71.8	310	4 AAB70842	Aab70842 SNV-env 1
3	1202.5	69.7	315	4 AAB70843	Aab70843 SNV-env 1
4	1186.5	68.8	309	4 AAB70841	Aab70841 SNV-env 1
5	1098	63.7	291	6 ABR42054	AbR42054 Newcastle
6	1045.5	60.6	543	7 ADD12876	Add12876 CD28/mela
7	1004	58.2	302	4 AAB70844	Aab70844 SNV-env 1
8	993.5	57.6	729	4 AAB20439	Aab20439 Antibody
9	992.5	57.5	231	4 AAB20443	Aab20443 Antibody
10	992.5	57.5	322	4 AAB20440	Aab20440 Antibody
11	991	57.4	298	8 ADS88777	Ads88777 Amino aci
12	991	57.4	554	3 AAY50822	Aay50822 Fv-antibo
13	983	57.0	305	3 AAY51142	Aay51142 Murine de
14	983	57.0	305	3 AAY59265	Aay59265 Antibody
15	978	56.7	260	2 AAW95600	Aaw95600 Anti-digo
16	978	56.7	260	2 AAW89101	Aaw89101 Anti-digo
17	974.5	56.5	562	6 ABR57059	AbR57059 Plasmid p
18	948.5	55.0	500	7 ADD13792	Add13792 Plasmid p
19	947.5	54.9	252	4 AAU07497	Aau07497 Synthetic
20	946.5	54.9	271	2 AAW02293	Aaw02293 FvKC-II-K
21	935.5	54.2	239	4 AAB47111	Aab47111 scFv 508F
22	935.5	54.2	239	6 AAO16066	Aao16066 Human neu
23	935.5	54.2	239	8 ADJ88113	Adj88113 Human bet
24	927	53.7	261	8 ADT91213	Adt91213 Single ch
25	924	53.6	331	6 AAE37727	Aae37727 Chemokine

26	924	53.6	732	4 AAB20437	Aab20437 Anti-FIX/
27	923.5	53.5	577	4 AAB19872	Aab19872 Activatin
28	923	53.5	267	3 AAB09776	Aab09776 TMV 30K m
29	923	53.5	294	4 AAB20442	Aab20442 Anti-FIX/
30	922.5	53.5	709	8 ADR43337	Adr43337 Anti-NKG2
31	920	53.3	555	4 AAB19871	Aab19871 Activatin
32	920	53.3	565	4 AAB19873	Aab19873 Activatin
33	919	53.3	325	4 AAB20438	Aab20438 Anti-FIX/
34	918.5	53.2	257	2 AAY05363	Aay05363 HBV speci
35	918.5	53.2	580	2 AAW90217	Aaw90217 Bispecific
36	918	53.2	895	5 AAU75369	Aau75369 Diphtheri
37	918	53.2	895	5 AAU75368	Aau75368 Diphtheri
38	918	53.2	895	5 AAU75374	Aau75374 Diphtheri
39	918	53.2	895	6 AAO29673	Aao29673 Anti-T ce
40	918	53.2	896	5 AAU75367	Aau75367 Diphtheri
41	918	53.2	896	5 AAU75366	Aau75366 Diphtheri
42	918	53.2	896	5 AAU75373	Aau75373 Diphtheri
43	918	53.2	896	6 AAO29672	Aao29672 Anti-T ce
44	918	53.2	896	6 AAO29671	Aao29671 Anti-T ce
45	918	53.2	896	6 AAO29676	Aao29676 Anti-T ce

ALIGNMENTS

RESULT 1
AAB70840
ID AAB70840 standard; protein; 329 AA.
XX AC AAB70840;
XX AC
DT 11-SEP-2003 (revised)
DT 25-JUN-2001 (first entry)
XX
DE SNV-env leader/human 7A5-scFv fusion construct.
XX
KW T lymphocyte; antibody; single chain variable antibody; scFv; human;
KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
KW acquired immune deficiency syndrome; severe combined immune deficiency;
KW T cell lymphoma; fusion construct.
XX
OS Homo sapiens.
OS Spleen necrosis virus.
OS Chimeric.
XX
XX Key Location/Qualifiers
FT Protein 1..45
FT Protein /label= SNV-env_leader
FT Protein 46..329
FT Protein /label= 7A5-scFv
DE19946142-A1.
PD 29-MAR-2001.
XX
PF 27-SEP-1999; 99DE-01046142.
XX
XX 27-SEP-1999; 99DE-01046142.
PR (BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
XX
XX Cichutek K, Engelstaedter M;
XX WPI; 2001-246140/26.
DR N-PSDB; AAP61509.
XX
XX Cell-targeting vector selective for T lymphocytes, useful in gene therapy
XX of e.g. acquired immune deficiency syndrome, encodes a single-chain
XX variable antibody fragment.
PS Claim 1; Fig 1; 18pp; German.
XX

CC This invention describes a novel cell-targeting vector (A) containing a
CC DNA sequence (I) encoding a single-chain variable antibody fragment
CC (scFv). The products of the invention have antiviral, cytostatic and
CC immunostimulant activity and can be used in gene therapy, immunization
CC and diagnosis particularly of T cell-associated diseases, specifically
CC acquired immune deficiency syndrome (AIDS), severe combined immune
CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
CC human B cells, and 1000 fold selectivity over other human cells. A vector
CC designated 7A5 encodes a 329 amino acid single-chain variable antibody
CC fragment, fully defined in the specification. It was used to transform
CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
CC (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
CC carcinoma) cells. After 48 hours, the cells were stained with X-gal to
CC determine transformation. The viral titer (infectious units/ml) was over
CC 1 million for D17, 1 million for C8166 but less than 100 for HeLa,
CC showing the high selectivity for human T cells. This sequence represents
CC the SNV-env leader/human 7A5-scFv fusion construct used in the
CC construction of novel cell targeting vectors described in the invention.
CC (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 329 AA;

Query Match 100.0%; Score 1725; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 2e-97;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDCLTNLSAEGKVDQASKILLVAVWVGFTTAEVSTARAAPAAAEVKLQSGAELVR 60
DB 1 MDCLTNLSAEGKVDQASKILLVAVWVGFTTAEVSTARAAPAAAEVKLQSGAELVR 60
QY 61 PGVSVKLSCKGSGYTFDYGMVWVKQSHAKSLEWIGLISYYGDPVSNQRFKGAITMVD 120
DB 61 PGVSVKLSCKGSGYTFDYGMVWVKQSHAKSLEWIGLISYYGDPVSNQRFKGAITMVD 120
QY 121 KSNNTAYLEARLTSEDSAIYCARSDNGYGYVALDYWGQTTVTVSSGGSGGGGG 180
DB 121 KSNNTAYLEARLTSEDSAIYCARSDNGYGYVALDYWGQTTVTVSSGGSGGGGG 180
QY 181 GGGSDIELTQPSLSVLSLQORATISCRASESDVSDGSMFHWYQKPGPPKLLIYRAS 240
DB 181 GGGSDIELTQPSLSVLSLQORATISCRASESDVSDGSMFHWYQKPGPPKLLIYRAS 240
QY 241 NLESGVPARFSGSGESDFTLTIDPVEEDDAAVYICLQSMEDPYTFGGGTKLEIKRAAAS 300
DB 241 NLESGVPARFSGSGESDFTLTIDPVEEDDAAVYICLQSMEDPYTFGGGTKLEIKRAAAS 300
QY 301 GSGGGSGGGSGGGSGGGSGGGSGGASPVQFI 329
DB 301 GSGGGSGGGSGGGSGGGSGGGSGGASPVQFI 329

RESULT 2
AAB70842
ID AAB70842 standard; protein; 330 AA.
XX
AC AAB70842;
XX
DT 11-SEP-2003 (revised)
XX 25-JUN-2001 (first entry)
XX SNV-env leader/human 7B2-scFv fusion construct.
XX
DE T lymphocyte; antibody; single chain variable antibody; scFv; human;
KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
KW acquired immune deficiency syndrome; severe combined immune deficiency;
KW T cell lymphoma; fusion construct.
XX
OS Homo sapiens.
OS Spleen necrosis virus.
OS Chimeric.
XX

FH Key Location/Qualifiers
FT Protein 1. .45
FT /label= SNV-env_leader
FT Protein 46. .330
FT /label= 7B2-scFv
XX
PN DE19946142-A1.
XX
PD 29-MAR-2001.
XX
PF 27-SEP-1999; 99DE-01046142.
XX
PR 27-SEP-1999; 99DE-01046142.
XX
PA (BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
XX
PI Cichutek K, Engelstaedter M;
XX
DR WPI; 2001-246140/26.
DR N-PSDB; AAF61511.
XX
PT Cell-targeting vector selective for T lymphocytes, useful in gene therapy
PT of e.g. acquired immune deficiency syndrome, encodes a single-chain
PT variable antibody fragment.
XX
PS Claim 1; Fig 3; 18pp; German.
XX
CC This invention describes a novel cell-targeting vector (A) containing a
CC DNA sequence (I) encoding a single-chain variable antibody fragment
CC (scFv). The products of the invention have antiviral, cytostatic and
CC immunostimulant activity and can be used in gene therapy, immunization
CC and diagnosis particularly of T cell-associated diseases, specifically
CC acquired immune deficiency syndrome (AIDS), severe combined immune
CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
CC human B cells, and 1000 fold selectivity over other human cells. A vector
CC designated 7A5 encodes a 329 amino acid single-chain variable antibody
CC fragment, fully defined in the specification. It was used to transform
CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
CC (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
CC carcinoma) cells. After 48 hours, the cells were stained with X-gal to
CC determine transformation. The viral titer (infectious units/ml) was over
CC 1 million for D17, 1 million for C8166 but less than 100 for HeLa,
CC showing the high selectivity for human T cells. This sequence represents
CC the SNV-env leader/human 7B2-scFv fusion construct used in the
CC construction of novel cell targeting vectors described in the invention.
CC (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 330 AA;

Query Match 71.8%; Score 1239; DB 4; Length 330;
Best Local Similarity 73.2%; Pred. No. 7.9e-68;
Matches 243; Conservative 30; Mismatches 45; Indels 14; Gaps 5;
QY 1 MDCLTNLSAEGKVDQASKILLVAVWVGFTTAEVSTARAAPAAAEVKLQSGAELVR 60
DB 1 MDCLTNLSAEGKVDQASKILLVAVWVGFTTAEVSTARAAPAAAEVKLQSGAELVR 60
QY 61 PGVSVKLSCKGSGYTFDYGMVWVKQSHAKSLEWIGLI--STVYGPSPNQRFKGAITMT 118
DB 61 PGASVMSCKASGYAFTTYMHVWVKORPGGLEWIGYINPTDITD--YNLKFDKATLT 118
QY 119 VDKSSNTAYLEARLTSEDSAIYCARSDNGYGYVALDYWGQTTVTVSSGGSGGGGG 178
DB 119 ADKSSSTAYMQLSSLTSEDSAVYICARS---GWSYAMDYWGQTTVTISSGGSGGGGG 174
QY 179 SGGGGSDIELTQPSLSVLSLQORATISCRASESDVSDGSMFHWYQKPGPPKLLIYR 238
DB 175 SGGGGSDIELTQPSLSVLSLQORATISCRASESDVSDGSMFHWYQKPGPPKLLIYR 229
QY 239 ASNLESGVPARFSGSGESDFTLTIDPVEEDDAAVYICLQSMEDPYTFGGGTKLEIKRAA 298
DB 230 TSNLASGVPARFSGSGSGTSISLTISRMEADANTYTCQORSSYPPTFGSGTKLEIKRAA 289

CC activated T cells is required, so proliferation of T cells is not
CC limited. The antibodies of the invention are useful for treating cells to
CC effect supra-agonistic tumour cell-induced activation of T cells such
CC that no additional exogenous stimulus is required. The antibodies are
CC cytostatic and are useful for the treatment and prevention of tumours.
CC This sequence represents the bispecific antibody constructed from CD28
CC and a melanoma-associated proteoglycan.
XX
SQ Sequence 543 AA;

Query Match 60.6%; Score 1045.5; DB 7; Length 543;
Best Local Similarity 72.2%; Pred. No. 7.7e-56;
Matches 205; Conservative 25; Mismatches 41; Indels 13; Gaps 3;

Qy 27 WNGFGTTAEVSTARAQAPAM-----AEYKLOQSGAELVPGVSVKISKSGGYTF 76
Db 256 YMGQGTITVTSSASTKGPVFLAPSSSGSGQVKLOQSGPELVKPGASVKISKASGYAF 315

Qy 77 TDYGSMSVVKQSHAKSLEWIGLSTYYGDPSPYNORFKGKATMTYDKSNNTAYLRLTSE 136
Db 316 SRSWMNVVQRPQGLEWIGRIYPGDGTNYNGKFKGKATLTADKSSSTAYMQVSSLTSV 375

Qy 137 DSAIYYCARSDGNYGY-YALDYWGQGTITVTSSSGSGSGSGSGSGSDIELTQSPSSL 195
Db 376 DSAVYFCAR--GNTVVVPYTM DYWGQGTITVTSSSGSGSGSGSGSGSDIELTQSPASL 433

Qy 196 AVSLGORATISCRASESDSYGDSFMHWYQQKPGQPPLLIYPASNLGSGVPAFSGSGS 255
Db 434 AVSLGORATISCRASESDSYGNSFMHWYQQKPGQPPLLIYLASNLSGVPARFSGSGS 493

Qy 256 ESDFTLTIDPVEDDAVYCIQSMEDPYTFGGGTKLEIKRAAA 299
Db 494 RTDFTLTIDPVEDDAVYCIQSMEDPYTFGGGTKLEIKRAAA 537

RESULT 7
AAB70844
ID AAB70844 standard; protein; 302 AA.
XX
AC AAB70844;
XX
DT 11-SEP-2003 (revised)
DT 25-JUN-2001 (first entry)
XX
DE SNV-env leader/human 6C3-scFv fusion construct.
XX
KW T lymphocyte; antibody; single chain variable antibody; scFv; human;
KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
KW acquired immune deficiency syndrome; severe combined immune deficiency;
KW T cell lymphoma; fusion construct.
XX
OS Homo sapiens.
OS Spleen necrosis virus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Protein 1..45 /label= SNV-env_leader
FT Protein 46..302
FT Protein /label= 6C3-scFv
XX
PN DE19946142-A1.
XX
XX 29-MAR-2001.
XX
PF 27-SEP-1999; 99DE-01046142.
XX
PR 27-SEP-1999; 99DE-01046142.
XX
PA (BUND) BUNDESREPUBLIK DEUT PAUL-BEHLICH-INST.
XX
PI Cichutek K, Engelstaedter M;

RESULT 6
ADD12876
ID ADD12876 standard; protein; 543 AA.
XX
AC ADD12876;
XX
DT 01-JAN-2004 (first entry)
XX
DE CD28/melanoma-associated proteoglycan bispecific antibody.
XX
KW antibody; bispecific; VH chain; VL chain; T cell receptor; CD28;
KW tumour antigen; variable domain; light chain; heavy chain; heavy domain;
KW single-chain Fv antibody; scFv; melanoma-associated proteoglycan;
KW HER-2/neu; CD20; T cell activation; cytostatic; tumour.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 21..132
FT /note= "VL 9.3 (CD28 derived fragment)"
FT Region 133..147
FT /note= "FL region"
FT Region 148..267
FT /note= "VH 9.3 (CD28 derived fragment)"
FT Region 268..286
FT /note= "L region"
FT Region 287..407
FT /note= "VH 9.2.27 (melanoma-associated proteoglycan
FT derived fragment)"
FT Region 408..422
FT /note= "FL region"
FT Region 423..543
FT /note= "VL 9.2.27 (melanoma-associated proteoglycan
FT associated fragment)"
XX
PN WO2003042231-A2.
XX
XX 22-MAY-2003.
XX
PD 09-NOV-2002; 2002WO-EP012545.
XX
XX 12-NOV-2001; 2001DE-01056482.
XX
PA (JUNG/) JUNG G.
PA (JUNG/) JUNG G.
XX
PI Jung G, Jung G;
XX
XX WPI; 2003-457489/43.
XX
XX New bispecific antibody, useful for inducing T cell mediated destruction
XX of tumor cells, has binding sites for tumor antigen and CD28 T cell
XX receptor.
XX
XX Example 1; Fig 1b; 33pp; German.
XX
XX This invention describes a novel bispecific antibody comprising one
XX binding site for the T cell receptor CD28 and a second for a tumour
XX antigen (TAG), where each binding site comprises the variable domains of
XX the light and heavy chains and the heavy domains are connected through a
XX peptide linker. The peptide linker includes at least part of the N-
XX terminus of the CH1 domain of human immunoglobulin G (IgG) and at least
XX part of the Fc region (or hinge region) is fused to one light
XX chain. A modified antibody contains both of the constant domains of a Fab
XX fragment specific for a tumour, fused to a single-chain Fv antibody
XX (scFv) fragment specific for CD28. Optionally the antibody is also
XX bivalent for TAG and then consists of two antibodies or has a scFv
XX specific for CD28 fused to both heavy chains of a complete anti-TAG
XX antibody. The bispecific antibody dimerises spontaneously, creating a
XX dimer with two binding sites for each antigen. TAG is melanoma-associated
XX proteoglycan, HER-2/neu or CD20. Particularly no stimulation of CTLA-4 on

XX WPI; 2001-246140/26.
DR N-PSDB; AAF61513.
XX
PT Cell-targeting vector selective for T lymphocytes, useful in gene therapy
PT of e.g. acquired immune deficiency syndrome, encodes a single-chain
PT variable antibody fragment.
XX
XX
PS Claim 1; Fig 5; 18pp; German.
XX
CC This invention describes a novel cell-targeting vector (A) containing a
CC DNA sequence (I) encoding a single-chain variable antibody fragment
CC (scFv). The products of the invention have antiviral, cytostatic and
CC immunostimulant activity and can be used in gene therapy, immunization
CC and diagnosis particularly of T cell-associated diseases, specifically
CC acquired immune deficiency syndrome (AIDS), severe combined immune
CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
CC human B cells, and 1000 fold selectivity over other human cells. A vector
CC designated 7A5 encodes a 329 amino acid single-chain variable antibody
CC fragment, fully defined in the specification. It was used to transform
CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
CC (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
CC carcinoma) cells. After 48 hours, the cells were stained with X-gal to
CC determine transfection. The viral titer (infectious units/ml) was over
CC 1 million for D17, 1 million for C8166 but less than 100 for HeLa,
CC showing the high selectivity for human T cells. This sequence represents
CC the SNV-env leader/human 6C3-scFv fusion construct used in the
CC construction of novel cell targeting vectors described in the invention.
CC (Updated on 11-SEP-2003 to standardise OS field)
XX
XX
SQ Sequence 302 AA;

Query Match 58.2%; Score 1004; DB 4; Length 302;
Best Local Similarity 63.6%; Pred. No. 1.5e-53;
Matches 196; Conservative 47; Mismatches 51; Indels 14; Gaps 4;

QY 1 MDCLTNLRSAGKGVDOASKLILLVAVWGFQTAEVSTARRAQAQMAEVKLQSGAELVR 60
DB 1 MDCLTNLRSAGKGVDOASKLILLVAVWGFQTAEVSTARRAQAQMAEVKLQSGAEMKK 60

QY 61 PGVSVKISCKSGGYTFDYDQMSVWYKQSHAKSLEWIGLIISTYDGPYNORFKGKATWVD 120
DB 61 PGESLKISCKFGFYDFSTYIAWVRQMPGKGLVYMGILYPGDSDTKYSPSFQGVITISAD 120

QY 121 KSNNTAYLELRLTSDSATYICARSDG-----NYGVYALDYWGQTTVTSSGGG 172
DB 121 KSISTAYLQWSSLKASDTAMYICARVSGYCSSTSCYDY-YYYYMDVWNGRGLTVTVSRGGG 179

QY 173 GSGGGSGGGSGDIETQSPSSLAVSLGQRATISCRASESVDSYDGSFMHWYQQKFGQPP 232
DB 180 GSGGGSGGGSGDIIVMTQSPSTLSASVGRVTVTCRASQINIW----LAWYQQKFGKAP 235

QY 233 KLIYIRASNLIESGVPAFSGSGSESTFTLIDPVEEDDAAYVYCLOSMEDPYTFGGGTKL 292
DB 236 KLIYIRASTLESVPFRSGSGSGTEFTLTISGLQPDFFASYIC-QRYSDWSFGQGTKL 294

QY 293 EIKRAAAS 300
DB 295 EIKRAAAS 302

RESULT 8
AAB20439
ID AAB20439 standard; protein; 729 AA.
XX
AC AAB20439;
XX
DT 21-JUN-2001 (first entry)
XX
DE Antibody 8860-alkaline phosphatase fusion protein.
XX
KW Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant;

KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
XX alkaline phosphatase.
OS Mus musculus.
OS Synthetic.
OS Escherichia coli.
OS Chimeric.
XX
XX
PH Key Location/Qualifiers
FT Peptide 1..22 /label= Signal_peptide
FT Protein 23..729 /label= Mature_protein
FT Protein 23..271 /label= scFv
FT Region 23..142 /label= VH
FT Peptide 142..156 /label= Linker
FT Region 157..368 /label= VL
FT Peptide 289..272 /label= Spacer
FT Protein 273..723 /label= Alkaline_phosphatase
FT Peptide 724..729 /label= His_tag
XX
PN W0200119992-A2.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000WO-EP008936.
XX
PR 14-SEP-1999; 99AT-00001576.
XX
XX (BAXT) BAXTER AG.
XX
XX Scheifflinger F, Kerschbaumer R, Falkner F, Dorner F;
XX
DR WPI; 2001-290358/30.
DR N-PSDB; AAF30729.
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX
XX Example 16; Fig 29; 138pp; English.
XX
XX The present sequence is that of a fusion protein comprising: a PelB
CC leader; a single chain Fv (scFv) derivative of antibody 8860 comprising
CC the heavy (VH) and light (VL) chain variable regions of antibody 8860
CC joined by an artificial, flexible linker peptide; Escherichia coli
CC alkaline phosphatase; and a C-terminal 6His affinity tail. The DNA was
CC used in the construction of a miniantibody construct (see AAF30730),
CC (which was used as negative control in determination of Factor VIII
CC FVIII)-like activity of a 198/B1 miniantibody. 198/B1 is an example of
CC anti-human Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the
CC invention. Anti-FIX/FIXa antibodies and their derivatives have FVIIIa
CC cofactor or FIXa activating activity. Administration leads to an increase
CC in the procoagulant activity of FIXa, even in the presence of FVIIIa
CC inhibitors. This allows for rapid blood coagulation even in the absence
CC of FVIII or FVIIIa, and in the case of FVIII inhibitor patients. The
CC antibodies and derivatives are used in a claimed pharmaceutical
CC composition for treating patients with blood coagulation disorders,
CC especially haemophilia A and haemorrhagic diathesis. The scFv-alkaline
CC phosphatase was expressed in E. coli. It exhibited no FVIII-like activity
XX
SQ Sequence 729 AA;

Query Match 57.6%; Score 993.5; DB 4; Length 729;
Best Local Similarity 75.0%; Pred. No. 1.5e-52;

```
Matches 195; Conservative 23; Mismatches 39; Indels 3; Gaps 2;
QY 41 AAQAPMAEVLQOSGAELVRPGVSVKISCKGSGYFTDYDGMVWKQSHAKSLEWIGLIST 100
DB 16 AAQAPMAEVLQOSGPELVPGASVKISCKASGYAFSSWMVWKQPGQGLEWIGRIYP 75
QY 101 YYGDPSPNORFKGKATMTVDKSSNTAYLELARLTSEDSAIYYCARSDGNYGYVALDYWG 160
DB 76 GNGDTNYNGKFKGKATLTADKSSSTAYMQLSSLTSVDSAVYFCA--DGNV-YYVANDYWG 132
QY 161 QGTTVTVSSGGSGGGGGSGGSDIELTQSPSLAVSLGQRATISCRASEVSDSYGDSF 220
DB 133 QGTSVTVSSGGSGGGGRASGGGSGQIVLTQSPASLAVSLGQRATISCRASKSVSTSGSY 192
QY 221 MHWYQOKPGOPPKLLIYRASNLSESGVPARFSGSGSDFTLTIDPVEEDAAVYVCLOSM 280
DB 193 MHWYQOKPGOPPKLLIYLASNLSESGVPARFSGSGGDTFTLNHPVEEDAAVYVCOHSR 252
QY 281 EDPYTFGGGTGLEIKRAAAS 300
DB 253 ELPRTFGGGTGLEIKRAAAA 272
RESULT 9
ID AAB20443
XX AAB20443 standard; protein; 291 AA.
AC AAB20443;
XX
XX 21-JUN-2001 (first entry)
DE Antibody 8860-myc-tag fusion.
XX
XX Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse; myc-tag.
XX
OS Mus musculus.
OS Synthetic.
OS Escherichia coli.
OS Chimeric.
XX
XX Key Location/Qualifiers
FT Peptide 1..22
FT /label= Signal_peptide
FT Protein 23..291
FT /label= Mature_protein
FT Protein 23..268
FT /label= scFv
FT Region 23..141
FT /label= VH
FT Peptide 142..156
FT /label= Linker
FT Region 157..268
FT /label= VL
FT Peptide 269..271
FT /label= Spacer
FT Protein 272..283
FT /label= Myc_tag
FT Peptide 284..285
FT /label= Spacer
FT Peptide 286..291
FT /label= His_tag
XX
XX WO200119992-A2.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000WO-EP008936.
XX
XX 14-SEP-1999; 99AT-00001576.
XX
XX (BAXT ) BAXTER AG.
XX
```

```
XX PI Scheiflinger F, Kerschbaumer R, Falkner F, Dorner F;
XX DR WPI; 2001-290358/30.
XX DR N-PSDB; AAF30734.
XX
XX PT New factor IX/factor IXa antibodies and their derivatives useful for
XX PT increasing amidolytic activity of factor IXa, and for treating blood
XX PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX
XX Example 18; Fig 35; 138pp; English.
XX
XX The present sequence is that of a fusion protein comprising: a PelB
XX leader; a single chain Fv (scFv) derivative of antibody 8860 comprising
XX the heavy (VH) and light (VL) chain variable regions of 8860 joined by an
XX artificial, flexible linker peptide; a spacer; a Myc-tag peptide; a
XX spacer; and a C-terminal 6His affinity tail. The construct was expressed
XX in Escherichia coli from vector pMycHis6 and used as negative control in
XX determinations of the Factor-VIII (FVIII)-like activity of a 198/BI scFv
XX also expressed from pMycHis6. 198/BI is an example of anti-human Factor
XX IX (FIX)/activated Factor IX (FIXa) antibodies of the invention. Anti-
XX FIX/FIXa antibodies and their derivatives, including scFv fragments, have
XX FVIIIa cofactor activity or FIXa activant activity of FIXa, even in the
XX presence of FVIIIa inhibitors. This allows for rapid blood coagulation
XX even in the absence of FVIII or FVIIIa, and in the case of FVIII
XX inhibitor patients. The antibodies and derivatives are used in a claimed
XX pharmaceutical composition for treating patients with blood coagulation
XX disorders, especially haemophilia A and haemorrhagic diathesis
XX
XX SQ Sequence 291 AA;
XX
XX Query Match 57.5%; Score 992.5; DB 4; Length 291;
XX Best Local Similarity 75.3%; Pred. No. 7.2e-53;
XX Matches 195; Conservative 22; Mismatches 39; Indels 3; Gaps 2;
QY 41 AAQAPMAEVLQOSGAELVRPGVSVKISCKGSGYFTDYDGMVWKQSHAKSLEWIGLIST 100
DB 16 AAQAPMAEVLQOSGPELVPGASVKISCKASGYAFSSWMVWKQPGQGLEWIGRIYP 75
QY 101 YYGDPSPNORFKGKATMTVDKSSNTAYLELARLTSEDSAIYYCARSDGNYGYVALDYWG 160
DB 76 GNGDTNYNGKFKGKATLTADKSSSTAYMQLSSLTSVDSAVYFCA--DGNV-YYVANDYWG 132
QY 161 QGTTVTVSSGGSGGGGGSGGSDIELTQSPSLAVSLGQRATISCRASEVSDSYGDSF 220
DB 133 QGTSVTVSSGGSGGGGRASGGGSGQIVLTQSPASLAVSLGQRATISCRASKSVSTSGSY 192
QY 221 MHWYQOKPGOPPKLLIYRASNLSESGVPARFSGSGSDFTLTIDPVEEDAAVYVCLOSM 280
DB 193 MHWYQOKPGOPPKLLIYLASNLSESGVPARFSGSGGDTFTLNHPVEEDAAVYVCOHSR 252
QY 281 EDPYTFGGGTGLEIKRAAAA 299
DB 253 ELPRTFGGGTGLEIKRAAA 271
RESULT 10
AAB20440
ID AAB20440 standard; protein; 322 AA.
XX
XX AAB20440;
XX
XX 21-JUN-2001 (first entry)
XX
XX Antibody 8860 bivalent miniantibody.
XX
XX Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant;
KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
XX bivalent antibody.
XX
XX Mus musculus.
XX
```

OS Synthetic.
OS Escherichia coli.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= Signal_peptide
FT /note= "PelB leader"
FT Protein 23..322
FT /label= Mature_protein
FT Protein 23..268
FT /label= scFv
FT Region 23..141
FT /label= VH
FT Peptide 142..156
FT /label= Linker
FT Region 157..268
FT /label= VL
FT Peptide 269..271
FT /label= Spacer
FT Protein 272..281
FT /label= Hinge
FT Protein 282..316
FT /label= Helix
FT Peptide 317..322
FT /label= His_tag
XX
PN WO200119992-A2.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000WO-EP008936.
XX
XX 14-SEP-1999; 99AT-00001576.
XX (BAXT) BAXTER AG.
XX
XX Scheifflinger F, Kerschbaumer R, Falkner F, Dorner F;
XX
XX WPI; 2001-290358/30.
DR N-PSDB; AAF30730.
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX
XX Example 16; Fig 30; 138pp; English.
XX
XX The present sequence is that of a bivalent miniantibody comprising a PelB
CC leader peptide, the single chain Fv (scFv) fragment of antibody 8860, an
CC amphipathic helical structure and a C-terminal 6His tag. The protein was
CC expressed in Escherichia coli from plasmid p8860-Zip#1.2 (see AAF30730).
CC It was used as negative control in determinations of the factor VIII
CC (FVIII)-like activity of a 198/B1 miniantibody (see AAB20438). 193/B1 is
CC an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)
CC antibodies of the invention. Anti-FIX/FIXa antibodies and their
CC derivatives have FVIIIa cofactor activity or FIXa activating activity.
CC Administration leads to an increase in the procoagulant activity of FIXa,
CC even in the presence of FVIIIa inhibitors. This allows for rapid blood
CC coagulation even in the absence of FVIII or FVIIIa, and in the case of
CC FVIII inhibitor patients. The antibodies and derivatives are used in a
CC claimed pharmaceutical composition for treating patients with blood
CC coagulation disorders, especially haemophilia A and haemorrhagic
CC diathesis. The present bivalent miniantibody exhibited no FVIII-like
CC activity
XX
SQ Sequence 322 AA;
Query Match 57.5%; Score 992.5; DB 4; Length 322;
Best Local Similarity 75.3%; Pred. No. 8e-53;
Matches 199; Conservative 22; Mismatches 39; Indels 3; Gaps 2;
XX 41 AAQPAMAEVQLQSGPELVKPGASVKISKSGYAFSSWMNWVKQRPQGLEWIGRIYP 100

Db 16 AAQPAMAEVQLQSGPELVKPGASVKISKSGYAFSSWMNWVKQRPQGLEWIGRIYP 75
Qy 101 YYGDPSTYNORFKGKATMTVDKSNATAYLELRLTSEDSAIYYCARSDGNYGYAYLDYWG 160
Db 76 GNGDTNYNGKFKGKATLTADKSSSTAYMQLSSTSVDSAIFYFCA--DGNV-YYYAMDYWG 132
Qy 161 QGTTVTVSSGGGGSGGGGGSDIELTQSPSSSLAVSLGQRATISCRASESVDSYGDSEF 220
Db 133 QGTSVTVSSGGGGSGGGGGQIVLTQSPASLAVSLGQRATISCRASKSVSTSGSY 192
Qy 221 MEWYQKQPPKLLIYRASNLSEGVPAFPFSGSGSEDFTLTIDPVEEDAAVYICLSM 280
Db 193 MEWYQKQPPKLLIYLASNLSEGVPAFPFSGSGSGTDTLTINHPVEEDAAVYICQHSR 252
Qy 281 EDPYTFGGGTGLEIKRAAA 299
Db 253 ELPTFGGGTGLEIKRAAA 271
RESULT 11
ADS88777
ID ADS88777 standard; protein; 298 AA.
XX
AC ADS88777;
XX
XX 16-DEC-2004 (first entry)
XX
XX Amino acid sequence of the IC2 scFv antibody from clone p330.
DE
XX
XX G glycoprotein; respiratory syncytial virus;
KW respiratory syncytial virus infection; RSV; RSV infection; IC2; scFv.
XX
XX Mus sp.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Peptide 1..22
FT /note= "PelB leader sequence"
FT Region 144..158
FT /note= "linker"
FT Region 276..281
FT /note= "His tag"
FT Region 285..295
FT /note= "cmcy tag"
XX
XX WO2004083373-A2.
XX
XX 30-SEP-2004.
XX
XX 22-MAR-2004; 2004WO-GB0001239.
XX
XX 22-MAR-2003; 2003GB-00006618.
XX (UYNE-) UNIV NEWCASTLE-UPON-TYNE.
XX
XX Toms G, Routledge E, Mekseepalard C;
XX
XX WPI; 2004-691033/67.
DR N-PSDB; ADS88776.
XX
XX New antibody against the G glycoprotein of RSV with a variable region
PT having a first and second domain from a VL and VH region, respectively,
PT useful for treating respiratory syncytial virus (RSV) infections.
XX
XX Example 2; SEQ ID NO 45; 93pp; English.
XX
XX The specification describes an against the G glycoprotein of respiratory
CC syncytial virus, with a variable region comprising a first domain from a
CC variable light chain region and a second domain a variable heavy chain
CC region. The antibodies of the invention are useful for treating and
CC preventing the development of infections caused by the respiratory
CC syncytial virus (RSV). The present sequence represents the IC2 scFv from

CC collection of hematopoietic undifferentiated cells, elimination of
CC lymphocytes from cells to be used in bone marrow transplantation, the
CC detection of leukemic cells and the production of medicinal compositions
CC for the treatment of HIV infection and autoimmune diseases. This sequence
CC represents a murine derived protein fragment which is used to illustrate
CC the method of the invention
XX
SQ Sequence 305 AA;

Query Match 57.0%; Score 983; DB 3; Length 305;
Best Local Similarity 73.3%; Pred. No. 2.9e-52;
Matches 189; Conservative 26; Mismatches 39; Indels 4; Gaps 1;
QY 41 AAQPAVAEVLQOSGAELVRPGVSVKISCKGSGYTFTDYGMSVVKQSHAKSLEWIGL1ST 100
DB 16 AAQPAVAQVLQOSGPELVKPGASVMSCKASGYTFTDVIWNLNORTQCGLEWIGE1P 75
QY 101 YYGDPSPNORFKGATMTVDKSNNTAYLELRLTSEDSAIYYCARSDGNGYVYALDYWG 160
DB 76 GSGSAYYNEFMFKGATLTADKSNNTAYMQLSSLTSEDSAVYFCARRGTGTGF---AYWG 131
QY 161 QGTTVTVSSGGSGGGGGGGSDIELTQSPSSLAIVSLGORATISCRASESVDSYGDSE 220
DB 132 RGLTVTVSAGGSGGGGGGGSDIVLTQSPASLAVSLGORATISCKASQSDYDGDY 191
QY 221 MHVYQKPGQPKLLIYRASNLSEGVPARFSGSGSDFTLTIDPVEEDDAVYVYCLQSM 280
DB 192 MNWYQKPGQPKLLIYAAASNLSEGIPIARFSGSGGTFTLNIHPVEEDDAATYYCQSS 251
QY 281 EDPYTFGGGTGLEIKRAA 298
DB 252 EDPPTFGGGTGLEIKAAA 269

RESULT 14
AAV5265
ID AAV5265 standard; protein; 305 AA.

XX AAV5265;
XX
XX 17-APR-2000 (first entry)
XX Antibody 4H5 L chain sequence.
XX CD4 antigen; anti-human; antibody; 4H5; drug.
XX Mus sp.
XX JP11332563-A.
XX 07-DEC-1999.
XX 26-MAY-1998; 98JP-00163034.
XX 26-MAY-1998; 98JP-00163034.
XX (ASAH) ASAH KASEI KOGYO KK.
XX WPI; 2000-091351/08.
XX N-PSDB; AA258664.

XX An antibody and the nucleic acid coding the antibody.
XX Disclosure; Page 17-18; 25pp; Japanese.

XX The invention provides an antibody having affinity to CD4 antigen. The
XX anti-human CD4 antibody 4H5 is used for the detection of antigen and
XX application for drugs. It is highly safe in human dose. The present
XX sequence represents the L chain sequence of the antibody 4H5
XX
SQ Sequence 305 AA;

Query Match 57.0%; Score 983; DB 3; Length 305;

Best Local Similarity 73.3%; Pred. No. 2.9e-52;
Matches 189; Conservative 26; Mismatches 39; Indels 4; Gaps 1;
QY 41 AAQPAVAEVLQOSGAELVRPGVSVKISCKGSGYTFTDYGMSVVKQSHAKSLEWIGL1ST 100
DB 16 AAQPAVAQVLQOSGPELVKPGASVMSCKASGYTFTDVIWNLNORTQCGLEWIGE1P 75
QY 101 YYGDPSPNORFKGATMTVDKSNNTAYLELRLTSEDSAIYYCARSDGNGYVYALDYWG 160
DB 76 GSGSAYYNEFMFKGATLTADKSNNTAYMQLSSLTSEDSAVYFCARRGTGTGF---AYWG 131
QY 161 QGTTVTVSSGGSGGGGGGGSDIELTQSPSSLAIVSLGORATISCRASESVDSYGDSE 220
DB 132 RGLTVTVSAGGSGGGGGGGSDIVLTQSPASLAVSLGORATISCKASQSDYDGDY 191
QY 221 MHVYQKPGQPKLLIYRASNLSEGVPARFSGSGSDFTLTIDPVEEDDAVYVYCLQSM 280
DB 192 MNWYQKPGQPKLLIYAAASNLSEGIPIARFSGSGGTFTLNIHPVEEDDAATYYCQSS 251
QY 281 EDPYTFGGGTGLEIKRAA 298
DB 252 EDPPTFGGGTGLEIKAAA 269
RESULT 15
AAW95600
ID AAW95600 standard; protein; 260 AA.
XX AAW95600;
XX
XX 31-MAR-1999 (first entry)
XX Anti-digoxin scFv antibody fragment.
XX Immunoassay; analyte; anti-analyte antibody; bacterial; anti-digoxin;
XX single chain Fv; scFv.
XX Synthetic.
XX Key Location/Qualifiers
XX Peptide 1..119
XX Peptide /note= "Variable heavy chain"
XX Peptide 120..134
XX Peptide /note= "linker peptide"
XX Peptide 135..260
XX Misc-difference 136 /note= "variable light chain"
XX Misc-difference 138 /note= "indicated as Val in Fig 1"
XX Misc-difference 139 /note= "indicated as Met in Fig 1"
XX Misc-difference 141 /note= "indicated as Thr in Fig 1"
XX Misc-difference 143 /note= "indicated as Leu in Fig 1"
XX Misc-difference 146 /note= "indicated as Pro in Fig 1"
XX Misc-difference 151 /note= "indicated as Asp in Fig 1"
XX Misc-difference 152 /note= "indicated as Gln in Fig 1"
XX Misc-difference 154 /note= "indicated as Ser in Fig 1"
XX Misc-difference 176 /note= "indicated as Leu in Fig 1"
XX Misc-difference 179 /note= "indicated as Ala in Fig 1"
XX Misc-difference 182 /note= "indicated as Ser in Fig 1"
XX Misc-difference 207 /note= "indicated as Gly in Fig 1"
XX Misc-difference 216 /note= "indicated as Arg in Fig 1"
XX

PN US5866344-A.
XX
PD 02-FEB-1999.
XX
PF 23-MAY-1995; 95US-00447402.
XX
PR 15-NOV-1991; 91US-00794731.
PR 10-JUN-1994; 94US-00258543.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Georgiou G;
XX
WPI: 1999-141920/12.
DR N-PSDB; AAX06088.
XX
XX Binding of analyte by antibody - expressed on surface of recombinant host cell.
XX
XX Example 1; Col 33-36; 33pp; English.
XX
CC The invention relates to novel competitive immunoassays that are useful in detecting and quantitatively measuring analytes. The immunoassays involve binding an analyte that comprises: (1) obtaining a host cell containing a vector and expressing an anti-analyte antibody or analyte-binding antibody fragment on the bacterial cell surface, and (2) contacting the cell with a sample containing the analyte. The method is useful for removing an analyte from a sample or for performing a competitive immunoassay in which the cell is contacted with the sample in the presence of a known amount of labelled analyte. Isolated and purified antibodies are not needed. The present sequence represents an anti-digoxin single chain Fv (scFv) antibody fragment
XX
SQ Sequence 260 AA;

Query Match 56.7%; Score 978; DB 2; Length 260;
Best Local Similarity 74.2%; Pred. No. 5e-52;
Matches 187; Conservative 30; Mismatches 31; Indels 4; Gaps 2;

QY 48 EVKLQSGAELVRPGVSVKISKSGYFTFDYGNVWKQSHAKSLEWIGLITYYGDPSY 107
DB 1 EVQLQSGPELVKPGASVVRMSCKSSGYFTDFYNNVVRQSHKSLDYIGYISPGVTGY 60

QY 108 NORFKGKATMTVDKSSNTAYLELARTSEDAIYCARSQDNYGYYYALDYWGQGTITTV 167
DB 61 NQPKGKATLTVDKSSSTAYWEIRLSLTSEDAVYICAGSSGN---KWAMDYWGHSATV 117

QY 168 SSGGGSGGGGGGGGGSDIELTQSPSLAVSLGORATISCRASES-VDSYGDSPFMHWYQQ 226
DB 118 SSGGGSGGGGGGGGGSDIVLTQSPASLAVSLGORATISCRSSQSLVHSGNTYLNWYQQ 177

QY 227 KPGQPPKLLIYRASNLESGVPARFSGSGSEDTLTIDPVEEDDAVYVYCLQSMEDPYTF 286
DB 178 KPGQPPKLLIYKVSNRPSGVPARFSGSGSEDTLTIDPVEEDDAIYVCSQTTHVPPTF 237

QY 287 GGGTKLEIKKAA 298
DB 238 GSGTKLELKRAS 249

Search completed: August 23, 2005, 12:27:13
Job time : 1535 secs

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OM protein - protein search, using sw model

Run on: August 23, 2005, 11:17:23 ; Search time 371 Seconds
(without alignments)
85.324 Million cell updates/sec

Title: US-10-089-278-6
Perfect score: 1725
Sequence: 1 MDCLTLNLSASGKVDQASKI.....GSGGGGGGGGSGASPQVFI 329
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	807	46.8	233	2 JC5322	p53 specific singl
2	798	46.3	249	2 S41374	single chain Fv an
3	783.5	45.4	268	2 A56446	Ig heavy chain V r
4	522	30.3	111	1 KWS37	Ig kappa chain V r
5	516	29.9	131	1 KWSM6	Ig kappa chain pre
6	500	29.0	136	1 HWSB1	Ig heavy chain pre
7	496	28.8	111	2 D45722	anti-glycoprotein
8	495	28.7	107	2 S26344	Ig kappa chain V r
9	493	28.6	115	2 S63596	Ig kappa chain V r
10	485	28.1	107	2 S26343	Ig kappa chain V r
11	485	28.1	112	2 S19976	Ig kappa chain V r
12	482	27.9	111	2 S09965	Ig kappa chain V r
13	480	27.8	111	2 E53285	Ig kappa chain V-J
14	480	27.8	132	1 KWSM32	Ig kappa chain V a
15	478	27.7	112	2 S19972	Ig kappa chain pre
16	477	27.7	137	2 H32513	Ig kappa chain pre
17	476	27.6	111	1 KWSM43	Ig kappa chain V r
18	475	27.5	111	1 KWSM08	Ig kappa chain V r
19	471	27.3	112	2 S19971	Ig kappa chain V r
20	470	27.2	111	1 KWSM31	Ig kappa chain V r
21	470	27.2	111	1 KWSM31	Ig kappa chain V r
22	470	27.2	131	2 PH1226	Ig kappa chain pre
23	468	27.1	111	1 KWSM59	Ig kappa chain V r
24	468	27.1	139	2 A27609	Ig heavy chain pre
25	468	27.1	150	2 F80444	Ig heavy chain V r
26	467	27.1	119	2 F30502	Ig heavy chain V r
27	465	27.0	210	2 A56169	Ig kappa chain V r
28	462.5	26.8	110	1 KWSM10	Ig kappa chain V r
29	461	26.7	111	1 KWSM40	Ig kappa chain V r

30	461	26.7	111	1 KWSM84	Ig kappa chain V r
31	460.5	26.7	119	2 PH0099	Ig heavy chain V r
32	460	26.7	111	1 KWSM80	Ig kappa chain V r
33	458.5	26.6	140	2 S04575	Ig heavy chain pre
34	457	26.5	111	2 S09969	Ig kappa chain V-J
35	455	26.4	111	1 KWSM50	Ig kappa chain V r
36	454	26.3	111	1 KWSM75	Ig kappa chain V r
37	454	26.3	111	2 PL0081	Ig kappa chain V r
38	454	26.3	114	2 S26319	Ig heavy chain V r
39	454	26.3	128	2 C37267	Ig heavy chain V r
40	453	26.3	111	1 KWSM85	Ig kappa chain V r
41	452.5	26.2	144	2 B30502	Ig heavy chain V r
42	448.5	26.0	140	2 T01407	Ig heavy chain (my
43	446	25.9	109	2 PH0093	Ig kappa chain V r
44	446	25.9	111	2 S09963	Ig kappa chain V-J
45	445.5	25.8	117	1 HWSM4E	Ig heavy chain V r

ALIGNMENTS

RESULT 1

JC5322
p53 specific single-chain antibody Pab421 - human
C:Species: Homo sapiens (man)
C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C:Accession: JC5322
R;Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A:Reference number: JC5322; MUID:97168950; PMID:9016757
A:Accession: JC5322
A:Molecule type: mRNA
A:Residues: 1-233 <JAN>
A:Experimental source: hydrioloma cell
C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 46.8%; Score 807; DB 2; Length 233;
Best Local Similarity 67.5%; Pred. No. 2.1e-41;
Matches 164; Conservative 20; Mismatches 49; Indels 10; Gaps 3;

Qy	52	QSGAELVRPGVSVKISKGGSGYFTDYGMWSVKQSHAKSLEWIGLSTVYGDPSNQRF	111
Db	1	QESGAELVRSGASVKLSCTTSGFNINDYMHVWKKRPEQGLEWIGRIDPENGDADMTRSS	60
Qy	112	KGKATMTVDKSSNTAYLELRLTSEDSAIYCARSDGNYYGYALDYMGQGTTVTVSSGG	171
Db	61	GVRATMTADTSSNTAYLQLSLTSEDVAVYVC-----NAG-----MDYWGQGTTVTVSSGG	111
Qy	172	GGSGGGGGGGGGDIETQSPSSLAVSLGORATISCRASESVDSYGSFMHWYQKPGQP	231
Db	112	GGSGGRASGGGGDIETQSPASLAVSLGORATISCRASKSVSTSGSYMHWNQKPGQP	171
Qy	232	PKLLIYRASNLSEGVPRFSGSGSEDPFTLTIDPVEEDDAVYVCLQSMEDPYFGGGTK	291
Db	172	PRLLIYLVNLESGVPRFSGSGSGDFTLNIHVEBEDAATYYC-QHIRELTSEGGTK	230
Qy	292	LEI 294	
Db	231	LEI 233	

RESULT 2

S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R;Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A:Description: Construction and functional characterization of a single chain Fv antibody
A:Reference number: S41374
A:Accession: S41374

	Matches	99;	Conservative	12;	Mismatches	15;	Indels	8;	Gaps	2;
Qy	36	VSTARAAQPMAAEVQLQQSGAELVRPGVSVKISKGSYFTFDYGHWKSHAKSLLEWI	95	:	: :	:	::: :: :	:		
Dd	11	VATATGVH---SQVLQQSGPEVVLRPGVSVKISKGSYFTTDYAHWWVKSHAKSLLEWI	67	:		:		:		
Qy	96	GLISTYVDPSYNQRFGKGATMTDKSSNTAYLLELARLTSEDAIYYCARSDGNYGYVA	155	:		:		:		
Dd	68	GWISTYNGNTSYNOKFKGKTMTVDKSSTVMHELARLTSEDSANLYCARYGNY----	122	:		:		:		
Qy	156	LDFWGGGTTVTSS	169	:		:		:		
Dd	123	FDFWGQTTLVTSS	136	:		:		:		
RESULT 7										
D45722 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 109) - C;Species: Mus musculus (house mouse) C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000 C;Accession: D45722 R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M. J. Virol. 67, 489-496, 1993 A>Title: Neutralizing monoclonal antibodies that distinguish three antigenic si A;Reference number: A45722; PMID:93100833; PMID:7677958 A;Accession: D45722 A>Status: preliminary; not compared with conceptual translation A:Molecule type: nucleic acid A;Residues: 1-111 <SIM> A>Note: sequence extracted from NCBI backbone (NCBIP:120592) C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: glycoprotein F;16-94/Domain: immunoglobulin homology <IMM>										
Query Match 28.8%; Score 496; DB 2; Length 111; Best Local Similarity 86.5%; Pred. NO. 3.le-23; Matches 96; Conservative 4; Mismatches 11; Indels 0; Gaps 0;										
Qy	185	DIETQSPLAVLSGRATISCRASESVDSYGDSPMHYWQKPQGPPKLLIYRASNLAS	244	:		:		:		
Dd	1	NIVLTQSPALSAVSRQRATISCRASESVDSYKSPMHYWQKPQGPPKLLIYLASNLES	60	:		:		:		
Qy	245	GVPAPRGSGSESDFTLITDPVEEDDAVYCLQSMEDPYTFGGGTKLBIK	295	:		:		:		
Dd	61	GVPTRPESGSGRTDTFLTIDPVEDADATVYCQNNEPRTPFGGTKLBIK	111	:		:		:		

```

RESULT      8
S263344
IG kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26344
R;StarK, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a p
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26344
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-107 <STA>
A;Cross-references: EMBL:X59209; NID:G52336; PIDN:CANA41919.1; PID:gl334074
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-93/Domain: immunoglobulin homology <IMM>

Query Match          28.7%; Score 495; DB 2; Length 107;
Best Local Similarity   87.6%; Pred. No. 3,5e-23;
Matches    92; Conservative     7; Mismatches    6; Indels    0; Gaps    0;

Qy       188 LTQPSSSLAVSIGQRATISCRASESVDSVGDSEFMHWYOKPGPKLLIYRASNLGGVP 247
         :|::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db        3 MTQTTPASLVSGQRATISCRASEVDVSNGSNFMHWYOKPGPKLLIYRASNLGGTIP 62

```


A;Cross-references: 1-111 <SAW>
A;Note: sequence extracted from NCBF backbone (NCBIN:63307, NCBIF:63311)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 27.8%; Score 480; DB 2; Length 111;
Best Local Similarity 80.9%; Pred. No. 2.8e-22;
Matches 89; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Qy 186 IELTQSPSSLAVALSGQRATISCRASESDVSGDSFMHWYQKPGQPPKLLIYRASNLKSG 245
Db 2 IIVTQSPASLAVALSGQRATISCRASESDVSGDSFMHWYQKPGQPPKLLIYFASNLKSG 61

Qy 246 VPARFSGSGSESDFTLTIDPVEEDAAVYVCLQSMEDPYTFGGGTKLEIKR 295
Db 62 VPARFSGSGSRTDFTLTIDPVEEDAAVYVCLQSMEDPYTFGGGTKLEIKR 111

RESULT 14
KVM332
Ig kappa chain precursor V regions (MOPC 321, TEPC 124) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 31-May-1979 #sequence_revision 31-May-1979 #text_change 09-Jul-2004
C;Accession: A90412; A90373; A90374; A01933
R;Burststein, Y.; Schechter, I.
Biochemistry 17, 2392-2400, 1978
A;Title: Primary structures of N-terminal extra peptide segments linked to the variable expression of immunoglobulin genes.
A;Reference number: A90412; MUID:78235887; PMID:98179
A;Contents: MOPC 321
A;Accession: A90412
A;Molecule type: protein
A;Residues: 1-37 <BUR>
A;Cross-references: UNIPROT:P01658
A;Note: this precursor was synthesized in a cell-free system directed by mRNA isolated from R;McKean, D.; Potter, M.; Hood, L.
Biochemistry 12, 749-759, 1973
A;Title: Mouse immunoglobulin chains. Partial amino acid sequence of a kappa chain.
A;Reference number: A90373; MUID:73140224; PMID:4120629
A;Contents: MOPC 321
A;Accession: A90373
A;Molecule type: protein
A;Residues: 21-132 <MCK>
A;Note: the partial sequence of the C region of this Bence Jones protein was also determined by R;McKean, D.; Potter, M.; Hood, L.
Biochemistry 12, 760-771, 1973
A;Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains was determined by R;McKean, D.; Potter, M.; Hood, L.
A;Reference number: A90374; MUID:73140225; PMID:4691517
A;Contents: TEPC 124
A;Accession: A90374
A;Molecule type: protein
A;Residues: 21-131 <MC2>
A;Note: the sequence is compatible with that of MOPC 321 except in having 47-Glx, 51-Trp and 112-Ile.
C;Comment: The MOPC 321 sequence is shown.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) and two identical heavy (lambda) chains. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-132/Product: Ig kappa chain V regions (MOPC 321, TEPC 124) #status predicted <MAT>
F;36-114/Domain: immunoglobulin homology <IMM>
F;43-112/Disulfide bonds: #status predicted

Query Match 27.8%; Score 480; DB 1; Length 132;
Best Local Similarity 72.4%; Pred. No. 3.3e-22;
Matches 84; Conservative 20; Mismatches 12; Indels 0; Gaps 0;

Qy 181 GGSDIELTQSPSSLAVALSGQRATISCRASESDVSGDSFMHWYQKPGQPPKLLIYRAS 240
Db 17 GSTGDIVLTQSPASLAVALSGQRATISCRASKSVNTYGNFPMZWYKPGZPPKLLIYRAS 76

Qy 241 NLESGVPARFSGSGSESDFTLTIDPVEEDAAVYVCLQSMEDPYTFGGGTKLEIKR 296
Db 77 NLZSGIPARFSGSGSRTBFTLTIDPVAZABDVATYFCZZSBZBPWTFGGGTKLEIKR 132

RESULT 15
S19972
Ig kappa chain V region (M-T321) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S19972
R;Weissenborn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A;Description: Structural characterization of CD4 mAb.
A;Reference number: S19963
A;Accession: S19972
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <WEI>
A;Cross-references: EMBL:X65094; MID:952290; PIDN:CAA46222.1; PID:952291
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 27.7%; Score 478; DB 2; Length 112;
Best Local Similarity 82.1%; Pred. No. 3.7e-22;
Matches 92; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Qy 185 DIELTQSPSSLAVALSGQRATISCRASESDVSGDSFMHWYQKPGQPPKLLIYRASNLK 244
Db 1 DIVLTQSPASLAVALSGQRATIFCRASQSDVNAISYHNTYQKPGQPPKLLIYAAANLES 60

Qy 245 GVPARFSGSGSESDFTLTIDPVEEDAAVYVCLQSMEDPYTFGGGTKLEIKR 296
Db 61 GIPARFSGSGSGTDFTLIDHPVEEDAAVYVCLQSMEDPYTFGGGTKLEIKR 112

Search completed: August 23, 2005, 11:23:48
Job time : 372 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 11:17:23 ; Search time 1917 Seconds
(without alignments)
87.884 Million cell updates/sec

Title: US-10-089-278-6
Perfect score: 1725
Sequence: 1 MDCLTLNLSRABGKVDQASKI.....GSGGGGGGGGGGASPVQFI 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	800.5	46.4	244	2	Q65ZC8
2	773.5	44.8	243	2	Q7TQM2
3	768.5	44.6	487	2	Q85ZL2
4	763	44.2	298	2	Q9QYF0
5	762.5	44.2	241	2	Q921A6
6	760.5	44.1	255	2	Q6KB05
7	744.5	43.2	240	2	Q65ZC9
8	744	43.1	248	2	Q85ZQ7
9	737	42.7	218	2	Q925S1
10	607	35.2	170	2	Q925S2
11	522	30.3	111	1	KV3H_MOUSE
12	517	30.0	111	1	KV3J_MOUSE
13	516	29.9	131	1	KV3I_MOUSE
14	501	29.0	111	1	KV3K_MOUSE
15	500	29.0	136	1	HV15_MOUSE
16	480	27.8	132	1	KV3F_MOUSE
17	476	27.6	111	1	KV3M_MOUSE
18	475	27.5	111	1	KV3O_MOUSE
19	472	27.4	111	2	Q811U6
20	470	27.2	111	1	KV3L_MOUSE
21	470	27.2	111	1	KV3N_MOUSE
22	470	27.2	111	2	Q920E9
23	469	27.2	112	1	KV3G_MOUSE
24	468	27.1	111	1	KV3Q_MOUSE
25	464.5	26.9	117	2	Q9QXE9
26	462.5	26.8	110	1	KV3P_MOUSE
27	462.5	26.8	470	2	Q7TMK1
28	461	26.7	111	1	KV3R_MOUSE
29	461	26.7	111	1	KV3T_MOUSE
30	460	26.7	111	1	KV3A_MOUSE
31	459	26.6	488	2	Q91W11

32	457	26.5	238	2	Q66JS7	Q66j87	mus	musculus
33	456.5	26.5	112	1	KV3B_MOUSE	P01655	mus	musculus
34	455	26.4	111	1	KV3D_MOUSE	P01977	mus	musculus
35	454	26.3	111	1	KV3S_MOUSE	P01671	mus	musculus
36	453.5	26.3	481	2	Q8VCV5	Q8vcv5	mus	musculus
37	453	26.3	111	1	KV3U_MOUSE	P01673	mus	musculus
38	452.5	26.2	117	2	Q9QXE0	Q9qxf0	mus	musculus
39	452.5	26.2	134	2	Q85ZR6	Q85zr6	mus	musculus
40	452	26.2	472	2	Q6PUA7	Q6pja7	mus	musculus
41	451	26.1	111	1	KV3C_MOUSE	P01656	mus	musculus
42	445.5	25.8	117	1	HV12_MOUSE	P01756	mus	musculus
43	442	25.6	118	1	HV51_MOUSE	P06330	mus	musculus
44	441.5	25.5	117	1	HV13_MOUSE	P01757	mus	musculus
45	437	25.3	111	1	KV3E_MOUSE	P01657	mus	musculus

ALIGNMENTS

RESULT 1
Q65ZC8 PRELIMINARY; PRT; 244 AA.
AC Q65ZC8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies."
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13057; CAA73500.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PSS0835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 244
SQ SEQUENCE 244 AA; 26127 MW; 481F17868339F2BF CRC64;

Query Match 46.4%; Score 800.5; DB 2; Length 244;
Best Local Similarity 60.6%; Pred. No. 3.8e-48;
Matches 151; Conservative 39; Mismatches 54; Indels 5; Gaps 2;

Qy	48	EVKLQSGAEIVRGVSVKISCKSGGYTFDYGNSWVKQSHAKSLEWIGLISITYGDP	SY 107
Db	1	QVQLVQSGAEVKGPGDSVKVSKASGYTFSDFHYMHVYRQAPQGQLEWGMIDP	NNGDTRF 60
Qy	108	NQRFKQATWTDKSNNTAYLELRLTSEDAIYICARSDGNYGYVALDYWGQTTVT	V 167
Db	61	AQRFQGVWTRDTSISAAVMEVSRLESDTAVYICAR-EGTGSATYGMVWGQTLTV	V 119
Qy	168	SSGGGGGGGGGGGGSDIELTQSPSLAVSLGQRATISCRASVSDSYGDSFHWYQ	QOK 227
Db	120	SSGGGGGGGGGGGGSDIQWTSPTLSASIGDRVITCRASGEIYHW----	LAWYQOK 175
Qy	228	PGQPKLLIIRANLSSGVPARFGSGSSEDFLTIDPVEDDAVYICLQSMEDPTFG	287
Db	176	PGKAPFLIYKASLSASGAPRFGSGSGGTDLTITSSLPQDFPATYCCQYSNYPL	TFG 235
Qy	288	GGTKLEIKR 296	
Db	236	GGTKLEIKR 244	

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RESULT 2
Q7TQM2
ID Q7TQM2 PRELIMINARY; PRT; 243 AA.
AC Q7TQM2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ScFv GH8 protein (Fragment).
GN Name=scFv 6H8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/C;
RX MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
RA Peter J.C., Eftekhari P., Billiard P., Wallukat G., Hoebeke J.;
RT "scfv single chain antibody variable fragment as inverse agonist for
RL the beta-2 adrenergic receptor.";
RL J. Biol. Chem. 278:36740-36747(2003).
DR EMBL; AJ574851; CAE00495.1; -.
DR HSSP; P01751; 1A6W.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON TER
SQ SEQUENCE 243 AA; 25976 MW; B5FF64D2DC4F76 CRC64;

Query Match 44.8%; Score 773.5; DB 2; Length 243;
Best Local Similarity 62.5%; Pred. No. 2.9e-46;
Matches 155; Conservative 32; Mismatches 50; Indels 11; Gaps 5;

Qy 48 EVKLQSCAEIVRQGVSVKISCKSGYFTFDYGMVSKQSHAKSLEWGLISTYVGPST 107
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 QVQLQSGSELVRPGASVKLSCKASGYFTFTYWHWVKQRHGGLEWIGNIYPGSGITNY 60
Qy 108 NQRFKQKATMTVDKSSNTAYLELRLTSEDAIYYCARSDGNYYGYALDYWGQGTITV 167
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 DEKFNKGLIVDTSSSTAYVHLSLASEDSAVYYCAR--GGRG---LDVWGAGTTLTV 114
Qy 168 SSGGGSGGGSGGGGGSDIELTQSPSLAVSLGQRATISCRASESVDSYGFHFWYQOK 227
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
115 SSGGGSGGGSGGGGGSDIQMTQSSSFVSLGDRVTITCKASE--DIY--NRLAWYQOK 170
Qy 228 PGQPPKLLIYRASNLSEGVPRFSGSGSEDFTLTIDPVEDDAVYYCLOSMEDPYTFG 287
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
171 PGNAPELLISGATSLQETGVPRFSGSGGKDYTLISITSLQTEDVATYYC-QQYWSRTFG 229
Qy 288 GGTGLEIK 295
Db :|||||:
230 GGTGLEIK 237

RESULT 3
Q65ZL2
ID Q65ZL2 PRELIMINARY; PRT; 487 AA.
AC Q65ZL2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE FV/M4.
GN Name=M4-IFN- $\tau$ au;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96272580; PubMed=8688499;

Qi Y., Xiang J.;
"A genetically engineered single-gene-encoded anti-TAG72 chimeric
antibody secreted from myeloma cells.";
Hum. Antibodies Hybridomas 6:161-166(1995).
DR EMBL; S82493; AAB37424.2; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 487 AA; 53578 MW; C7BAB69F30555504 CRC64;

Query Match 44.6%; Score 768.5; DB 2; Length 487;
Best Local Similarity 56.0%; Pred. No. 1.4e-45;
Matches 154; Conservative 42; Mismatches 60; Indels 19; Gaps 6;

Qy 27 W-WGFGTTAEVSTARRAAQPAWAEVKLQSCAEIVRPGVSVKISCKSGYFTFDYGMVSK 85
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3 WSWVLFLLSVTTG-----VHSVQVQSQDAELVPGASVKISCKASGYFTDTHAIHWAK 57
Qy 86 QSHAKSLEWGLISTYVGPSTYVNRPFKQKATMTVDKSSNTAYLELRLTSEDAIYYCAR 145
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
58 QKPEQGLEWIGYISPGNDDIKYNEKFKGKATLTADKSSSTAYVHQLNSLTSEDSAVYFCKR 117
Qy 146 SDGNYGYVYALDYWGQGTITVTVSSGGSGGGSGGGSDIELTQSPSSLAIVSLGQRATI 205
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
118 S-----YYG--HWGQGTTLT--GSGGGSGGGSGGGSGRIQMTQSPASLSVSVGELVTI 168
Qy 206 SCRASESVDSYGFHFWYQOKPGQPPKLLIYRASNLSEGVPRFSGSGSEDFTLTIDP 265
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
169 TCRASENIYGN-----LAWYQKQKSPQLLYVATNLADGVPRFSGSGSGTQYSLKINS 224
Qy 266 VEEDDAVYYCLOSMEDPYTFGGGTGLEIKRAAAS 300
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
225 LQSEDFSGSYCQHFQWGTPTFTFGGTRLEIKPRSKS 259

RESULT 4
Q9QYF0
ID Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CN 8 single chain antibody.
GN Name=CN 8 scFv;
OS synthetic construct.
OC other sequences; artificial sequences.
OX NCBI_TaxID=32630;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183931; PubMed=10706631; DOI=10.1073/pnas.050582197;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phase display subtraction
RT method.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR EMBL; AB036341; BAA88633.1; -.
DR PIR; A33933; A33933.
DR PIR; S19112; S19112.
DR HSSP; P01820; 1A7O.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 2.
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DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match
Best Local Similarity 44.2%; Score 763; DB 2; Length 298;
Matches 148; Conservative 40; Mismatches 63; Indels 8; Gaps 2;

Qy 41 AAQPMARVKKLQSGAELVRPGVSVKISKCKSGYFTFDYGMVWVKQSHAKSLEWIGLIST 100
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 33 AAQPMARVKKLQSGGLVRFPGSLKLSAASGDFSRVWMSWRQAPGKLEWIGEINP 92
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 101 YYGPPSYNQRFGKATMTVDKSSNTAYLELARLTSEDSAIYYCARSDGNYGYVALDYWG 160
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 93 DSSTINYTPSLKDKFIIISRDNAKNTLYLQMSKVRSEDTALYYCARA----SYIGHSAWG 148
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 161 QGTTVTSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 220
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 149 QGTTVTSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 204
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 221 MHWYQKPGQPKLLIYRASNLKESVVPARFSGSGSEDFTLTIDPVEEDDAAVYCLQSM 280
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 205 LAWYQKPGQPKLLIYRASNLKESVVPARFSGSGSEDFTLTIDPVEEDDAAVYCLQSM 280
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 281 EDPYTFGGGTGLEIKRAA 299
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 265 TTPYTFGGGTGLEIKRAA 283
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RL Mol. Cells 7:816-819(1997).
DR EMBL; U88067; AAB48044.1; -
DR PIR; S19865; S19865.
DR PIR; S19867; S19867.
DR PIR; S19868; S19868.
DR PIR; S26325; S26325.
DR HSP; P01607; I8WV.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 1
FT TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match
Best Local Similarity 44.2%; Score 762.5; DB 2; Length 241;
Matches 146; Conservative 44; Mismatches 47; Indels 17; Gaps 5;

Qy 48 EVKLQSGAELVRPGVSVKISKCKSGYFTFDYGMVWVKQSHAKSLEWIGLISTYGDPSY 107
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 1 QVKLQSGPELKEGTEVTKISKASGYFTFDYGMVWVKQAPGKLGKWMGINTTGEPT 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 108 NQRFGKATMTVDKSSNTAYLELARLTSEDSAIYYCARSDGNYGYVALDYWGQGTIVT 167
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 ADPFKRFAPFLETSASTAVLIQINNKEDTATYFCARKD----LLRYFDYWGQGTIVT 116
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match
Best Local Similarity 57.1%; Pred. No. 2e-45;
Matches 149; Conservative 38; Mismatches 55; Indels 13; Gaps 4;

Qy 48 EVKLQSGAELVRPGVSVKISKCKSGYFTFDYGMVWVKQSHAKSLEWIGLISTY----TY 102
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 1 QVKLQSGGLVRFPGSLKLSAASGDFSRVWMSWRQTPDKRLEWVAITSGGSYTY 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 103 GDPYNQRFGKATMTVDKSSNTAYLELARLTSEDSAIYYCARSDGNYGYVALDYWGQ 162
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 PD-----SVKGRFTISRDNAKNTLYLQMSLSKSEDTAMYYCARHI-NRYRDGAFDYWGQ 114
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 163 TTVTVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 220
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 115 TLTIVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 174
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 221 MHWYQKPGQPKLLIYRASNLKESVVPARFSGSGSEDFTLTIDPVEEDDAAVYCLQSM 280
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 175 LAWYQKPGQPKLLIYRASNLKESVVPARFSGSGSEDFTLTIDPVEEDDAAVYCLQSM 234
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 281 EDPYTFGGGTGLEIK 295
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 235 SYPLTFGAGTGLEIK 249
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
Q65ZC9 PRELIMINARY; PRT; 240 AA.
AC Q65ZC9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)

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DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1q/7;
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 240 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 43.2%; Score 744.5; DB 2; Length 240;
Best Local Similarity 57.4%; Pred. No. 3e-44;
Matches 143; Conservative 40; Mismatches 57; Indels 9; Gaps 2;

Qy 48 EVKLQSGAEIVRPGVSKISCKGSGYTFDYGMSWVKOSHAKSLEWIGLISITYGDPYS 107
Db 1 QVQLVQSGGGLVPGGSLRLSQAASGFTFSYGHVWRQAPGKLEWVAIVSDGSKYY 60

Qy 108 NQRFKQKATMTVDKSSNTAYLELARTSEDSAIYYCARSDGNYYGYVALDYWGQGTITVTV 167
Db 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCARDWGD----SLDPWGKGLTVTV 115

Qy 168 SSGGGSGGGSGGGGGSDIELTQSPSSLAIVLQORATISCRASVSDSYGDSFMHWYQK 227
Db 116 SSGGGSGGGSGGGGGSDIQWTSPLSASIGDRTVITCRASGIYRW----LAWYQK 171

Qy 228 PGQPPKLLIYRASNLSEGVPAFSGSGSESDFTLTIDPVEEDDAVYVYCLQSMEDPYTF 287
Db 172 PGKAPKLLIYKASLASRAPRFSGSGSGTDFTLTKISRVEADLGVYVYCFQSHVPTTF 231

Qy 288 GGTGLEIKR 296
Db 232 GGTGLEIKR 240

RESULT 8
Q65ZQ7
ID Q65ZQ7 PRELIMINARY; PRT; 248 AA.
AC Q65ZQ7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE B3(Fv)-PE40 (Fragment).
GN Name=B3(Fv)-PE40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92020904; PubMed=1924323;
RA Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;
RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete
regression of a human carcinoma in mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
DR EMBL; S57990; AAB19971.2; -.
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DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 248 248
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match 43.1%; Score 744; DB 2; Length 248;
Best Local Similarity 59.0%; Pred. No. 3.4e-44;
Matches 147; Conservative 37; Mismatches 61; Indels 4; Gaps 3;

Qy 48 EVKLQSGAEIVRPGVSKISCKGSGYTFDYGMSWVKOSHAKSLEWIGLISITYGDPYS 107
Db 2 DVKLVESSGGLVQPGGSLKLSCATSGTTFSDYYMYWRQTPKRLWEVAIVSNDSSAY 61

Qy 108 NQRFKQKATMTVDKSSNTAYLELARTSEDSAIYYCARSDGNYYGYVALDYWGQGTITVTV 167
Db 62 SDTVKGRTISRDNKNTLYLQMSRLKSEDTAIYSCARGLA-WGAWFA--YWGQGLTVTV 118

Qy 168 SSGGGSGGGSGGGGGSDIELTQSPSSLAIVLQORATISCRASE-SVDSYGDSFMHWYQK 226
Db 119 SSGGGSGGGSGGGGGSDVLTQSPSLPVSLLGDAQASISCRSQIIVHNGNTYLEMYLQ 178

Qy 227 KPGQPPKLLIYRASNLSEGVPAFSGSGSESDFTLTIDPVEEDDAVYVYCLQSMEDPYTF 286
Db 179 KPGQSPKLLIYKVSNRFPSPGVPDRFSGSGTDFTLTKISRVEADLGVYVYCFQSHVPTTF 238

Qy 287 GGTGLEIK 295
Db 239 GGTGLEIK 247

RESULT 9
Q925S1
ID Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
of the irradiated mice by treatment with the intestinal RNA of mice of
the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
DR HSSP; P01665; IQNZ.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 218 218
SQ SEQUENCE 218 AA; 527E4FA8F7982817 CRC64;

Query Match 42.7%; Score 737; DB 2; Length 218;
Best Local Similarity 64.4%; Pred. No. 9e-44;
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Matches 143; Conservative 31; Mismatches 44; Indels 4; Gaps 1;
QY 46 MAEYKLOQSGAELVRPGVSKISCKSGYTTDTYGMVSKVQSHAKSLEWIGLSTYYGDP 105
Db 1 MAQVKLOQSGPELKKPGTIVRISCKASGYTTTACGMQVQKMPGKGLKMGWINTHSGVP 60
QY 106 SYNORFKGATMTVDKSNNTAYLELRLTSDESAIYYCARSDGNVGYVYALDYWGQGTTV 165
Db 61 KYAEFGKRPAPFASLETASTAYLQISLNKEDTATYFCMRWDYDGGP-----AYWGQGTTV 116
QY 166 TVSSGGGGGGGGGGGGSDIELTQSPSLAVSLGQRATISCRASESVDSYGDSEFMHWYQ 225
Db 117 TVSSGGGGGGGGGGGGSDIVLTQSPASLAVSLGQRATISCRASESVDNIGISFMWYQ 176
QY 226 QKPGQPKLLIYRASNLGSGVPAFSGSGSESDFTLIDPVE 267
Db 177 QKPGQPKLLIYASKQSGVPAFSGSGSDTDFSLNIYPME 218

RESULT 10
Q925S2 PRELIMINARY; PRT; 170 AA.
AC Q925S2;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE MRP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL: AF240167; AAK43732.1; -.
DR HSP; P01751; IAGW.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;

Query Match 35.2%; Score 607; DB 2; Length 170;
Best Local Similarity 73.4%; Pred. No. 8e-35;
Matches 116; Conservative 17; Mismatches 21; Indels 4; Gaps 2;
QY 46 MAEYKLOQSGAELVRPGVSKISCKSGYTTDTYGMVSKVQSHAKSLEWIGLSTYYGDP 105
Db 1 MAQVKLOQSGPEVVRPGVSKISCKSGYTTDTYGMVSKVQSHAKSLEWIGLSTYDGT 60
QY 106 SYNORFKGATMTVDKSNNTAYLELRLTSDESAIYYCARSDGNVGYVYALDYWGQGTTV 165
Db 61 NYNOKFGKATMTVDKSNNTAYMELARLTSDSAIYYCARG-AYYGSFYFDYWGQGTTV 119
QY 166 TVSSGGGGGGGGGGGGSDIELTQSPSLAVSLGORA 203
Db 120 TVSSGGGGGGGGGGGGSE-----SSSPGGTKLEIKRAA 154

RESULT 11
KV3H_MOUSE
Matches 143; Conservative 31; Mismatches 44; Indels 4; Gaps 1;
QY 46 MAEYKLOQSGAELVRPGVSKISCKSGYTTDTYGMVSKVQSHAKSLEWIGLSTYYGDP 105
Db 1 MAQVKLOQSGPELKKPGTIVRISCKASGYTTTACGMQVQKMPGKGLKMGWINTHSGVP 60
QY 106 SYNORFKGATMTVDKSNNTAYLELRLTSDESAIYYCARSDGNVGYVYALDYWGQGTTV 165
Db 61 KYAEFGKRPAPFASLETASTAYLQISLNKEDTATYFCMRWDYDGGP-----AYWGQGTTV 116
QY 166 TVSSGGGGGGGGGGGGSDIELTQSPSLAVSLGQRATISCRASESVDSYGDSEFMHWYQ 225
Db 117 TVSSGGGGGGGGGGGGSDIVLTQSPASLAVSLGQRATISCRASESVDNIGISFMWYQ 176
QY 226 QKPGQPKLLIYRASNLGSGVPAFSGSGSESDFTLIDPVE 267
Db 177 QKPGQPKLLIYASKQSGVPAFSGSGSDTDFSLNIYPME 218

RESULT 12
KV3J_MOUSE
ID KV3J_MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-III region ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
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ID KV3H_MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-III region PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Galmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -1- MISCELLANEOUS: The PC 3741 and TEPC 111 sequences are identical.
DR PIR; A93204; KWS37.
DR HSP; P01665; IONZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
RW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Framework-3.
FT DOMAIN 93 101 Complementarity-determining-3.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 30.3%; Score 522; DB 1; Length 111;
Best Local Similarity 89.2%; Pred. No. 4.2e-29;
Matches 99; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 185 DIELTQSPSLAVSLGQRATISCRASESVDSYGDSEFMHWYQKPGQPKLLIYRASNL 244
Db 1 DIVLTQSPASLAVSLGQRATISCRASESVDSYGDSEFMHWYQKPGQPKLLIYRASNL 60
QY 245 GVPARFSGSGSESDFTLIDPVEEDAAVYVYCLQSMEDPYTFGGGTKEIK 295
Db 61 GIPARFSGSGSRDFTLTINPVEADVDVATYCCQSNEDPYTFGGGTKEIK 111

RESULT 12
KV3J_MOUSE
ID KV3J_MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-III region ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
```

"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.",
[2] Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).
SEQUENCE (PC 9245).
MEDLINE=79073152; PubMed=103003;
Weigert M., Gattamait L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin diversity";
Nature 276:785-790 (1978).
-I- MISCELLANEOUS: The ABPC22 and PC9241 sequences are identical.
HSSP; P01665; IONZ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS0835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN 1 23 Framework-1.
DOMAIN 24 38 Complementarity-determining-1.
DOMAIN 39 53 Framework-2.
DOMAIN 54 60 Complementarity-determining-2.
DOMAIN 61 92 Framework-3.
DOMAIN 93 101 Complementarity-determining-3.
DOMAIN 102 111 Framework-4.
DISULFID 23 92 By similarity.
NON_TER 111 111
SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;
Query Match 30.0%; Score 517; DB 1; Length 111;
Best Local Similarity 89.2%; Pred. No. 9.4e-29;
Matches 99; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
Qy 185 DIETQSPSSLAIVSLGQRATISCRASESVDSYGSFMHWYQKPGQPKLLIYASNLS 244
Db 1 NIVLTQSPASLAIVSLGQRATISCRASESVDSYGSFMHWYQKPGQPKLLIYASNLS 60
Qy 245 GVPAFSGSGSEDTLTIDPVEDDAAVYVYQKPGQPKLLIYASNLS 295
Db 61 GVPAFSGSGSRTDTLTIDPVEADDAATYVYQKPGQPKLLIYASNLS 111
RESULT 13
KV3I_MOUSE
ID_KV3I_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE OF 1-35.
RP MEDLINE=78235887; PubMed=981179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes";
RL Biochemistry 17:2392-2400 (1978).
RN [2]
RP SEQUENCE OF 21-131.
RP MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771 (1973).
RN [3]
RP REVISIONS.
RP MEDLINE=79012520; PubMed=99744;

McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).
HSSP; P01665; IONZ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS0835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region; Signal.
KW SIGNAL 1 20
FT CHAIN 21 131 Ig kappa chain V-III region MOPC 63.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 58 Complementarity-determining-1.
FT DOMAIN 59 73 Framework-2.
FT DOMAIN 74 80 Complementarity-determining-2.
FT DOMAIN 81 112 Framework-3.
FT DOMAIN 113 121 Complementarity-determining-3.
FT DOMAIN 122 131 Framework-4.
FT DISULFID 43 112 By similarity.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;
Query Match 29.9%; Score 516; DB 1; Length 131;
Best Local Similarity 86.1%; Pred. No. 1.3e-28;
Matches 99; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
Qy 181 GGGSDIELTQSPSSLAIVSLGQRATISCRASESVDSYGSFMHWYQKPGQPKLLIYAS 240
Db 17 GSGTGNIVLTQSPASLAIVSLGQRATISCRASESVDSYGSFMHWYQKPGQPKLLIYAS 76
Qy 241 NLESGVPARFSGSGSEDTLTIDPVEDDAAVYVYQKPGQPKLLIYAS 295
Db 77 NLESGVPARFSGSGSRTDTLTIDPVEADDAATYVYQKPGQPKLLIYAS 131
RESULT 14
KV3K_MOUSE
ID_KV3K_MOUSE STANDARD; PRT; 111 AA.
AC P01663;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region PC 4050.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE.
RP MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gattamait L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin diversity";
Nature 276:785-790 (1978).
HSSP; P01665; IONZ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS0835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
KW SIGNAL 1 23 Framework-1.
FT CHAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Framework-3.
FT DOMAIN 93 101 Complementarity-determining-3.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 111 111

SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;
Query Match 29.0%; Score 501; DB 1; Length 111;
Best Local Similarity 86.5%; Pred. No. 1.2e-27;
Matches 96; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
QY 185 DIETQSPSSLAIVSGQRATISCRASESVDSYGDSFMHWYQKQKQPPKLLIYRASNL 244
DB 1 NIVLTQSPASLAIVSGQRATISCRASESVDSYGDSFMHWYQKQKQPPKLLIYRASNL 60
QY 245 GVPARFSGSGSEFTLTIDPVEEDDAAYVYCLOSMDPYTFGGTKLEIK 295
DB 61 GVPARFSGSGSRDFTLTIDPVEADDAATYCCQNNEDPLTFGAGTKLEK 111
RESULT 15
HV15_MOUSE
ID HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
by a cloned B-cell lymphoma: a single copy of the VH gene is shared by
two adjacent CH genes."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC 1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00494; AAA38130.1; -;
DR PIR; A02042; HVMSB1.
DR HSSP; P01751; INQB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 Ig heavy chain V region BCL1.
FT DOMAIN 20 135 Ig-like.
FT NON TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64; .
Query Match 29.0%; Score 500; DB 1; Length 136;
Best Local Similarity 73.9%; Pred. No. 1.8e-27;
Matches 99; Conservative 12; Mismatches 15; Indels 8; Gaps 2;
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DB 11 VATATGVH---SQVLQSGSEVVRPGVSVKISCKGSGYFTFDYAMHWVVKQSHAKSLEWI 67
QY 96 GLISTYYGDPNSYNQRFKQKATMTYDKSNTAYLELRLTSDSAIYYCARSDGNYGYA 155
DB 68 GVIISTYNGTSYNQKFKGKATMTYDKSSSTVHMLARLTSDSANLYCARYGNY----- 122

QY 156 LDYWGQGTITVTSS 169
DB 123 FDYWGQGTITVTSS 136
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Job time : 1919 secs

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OM protein - protein search, using sw model

Run on: August 23, 2005, 11:17:23 ; Search time 318 seconds

(without alignments)

77.231 Million cell updates/sec

Title: US-10-089-278-6

Perfect score: 1725

Sequence: 1 MDCLTLNLRAGKVDQASKI.....GSGGGGGGGSGGASPVQFI 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	978	56.7	260	2	US-08-447-402-1
2	946.5	54.9	271	2	US-08-894-922A-10
3	923	53.5	267	4	US-09-419-788-30
4	918.5	53.2	297	4	US-09-486-814A-2
5	916.5	53.1	252	2	US-08-894-922A-14
6	914	53.0	269	3	US-09-070-408-132
7	908	52.6	673	3	US-09-423-439-32
8	894.5	51.9	273	2	US-08-403-853-18
9	878	50.9	288	3	US-09-423-439-38
10	873	50.6	353	4	US-09-203-958A-4
11	853.5	49.5	258	4	US-09-526-738A-4
12	844.5	49.0	256	4	US-09-526-738A-2
13	842	48.8	244	2	US-08-553-497A-20
14	837.5	48.6	239	2	US-08-553-497A-18
15	836.5	48.5	666	3	US-09-423-439-51
16	836	48.5	241	4	US-09-581-345-5
17	833.5	48.3	553	2	US-08-661-052-16
18	833.5	48.3	553	3	US-09-188-082-16
19	833.5	48.3	553	3	US-09-364-088-16
20	833.5	48.3	553	3	US-09-102-716-16
21	831	48.2	267	3	US-09-485-737B-2
22	831	48.2	267	4	US-10-071-485-2
23	826	47.9	240	1	US-08-488-113B-148
24	826	47.9	240	1	US-08-477-484B-148
25	826	47.9	240	2	US-08-646-360-148
26	826	47.9	240	3	US-08-839-765-148
27	826	47.9	240	3	US-09-136-389-148

28 826 47.9 240 3 US-09-610-838-148 Sequence 148, App
29 826 47.9 240 4 US-09-711-485-148 Sequence 148, App
30 825 47.8 246 2 US-08-553-497A-24 Sequence 24, Appl
31 823.5 47.7 239 3 US-08-279-772A-8 Sequence 8, Appl
32 823.5 47.7 239 3 US-08-902-486-11 Sequence 11, Appl
33 823 47.7 637 1 US-08-235-838-16 Sequence 16, Appl
34 823 47.7 637 2 US-08-465-473B-16 Sequence 16, Appl
35 822 47.7 244 2 US-08-553-497A-22 Sequence 22, Appl
36 821.5 47.6 252 1 US-08-133-804-4 Sequence 4, Appl
37 821.5 47.6 252 1 US-08-461-838-4 Sequence 4, Appl
38 821.5 47.6 252 2 US-08-461-386-4 Sequence 2, Appl
39 821.5 47.6 270 2 US-08-652-507-2 Sequence 2, Appl
40 820 47.5 244 4 US-09-244-369B-1 Sequence 1, Appl
41 820 47.5 244 4 US-09-940-391-1 Sequence 1, Appl
42 819 47.5 365 3 US-08-875-811-53 Sequence 53, Appl
43 818.5 47.4 240 4 US-10-092-246-36 Sequence 36, Appl
44 818.5 47.4 240 4 US-10-096-246A-37 Sequence 37, Appl
45 816.5 47.3 348 4 US-09-646-028-12 Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-08-447-402-1
; Sequence 1, Application US/08447402
; Patent No. 5866344
; GENERAL INFORMATION:
; APPLICANT: Iverson, Brent
; APPLICANT: Georgiou, George
; APPLICANT: Chen, Gang
; TITLE OF INVENTION: IMMUNOASSAY AND ANTIBODY SELECTION
; TITLE OF INVENTION: METHODS USING CELL SURFACE EXPRESSED
; LIBRARIES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,402
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/258,543
; FILING DATE: 10-JUN-1994
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/794,731
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UT584\KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-447-402-1

Query Match	56.7%	Score	978;	DB	2;	Length	260;
Best Local Similarity	74.2%;	Pred.	No. 2.5e-62;				
Matches	187;	Conservative	30;	Mismatches	31;	Indels	4;
Gaps	2;						
Qy	48	EVLQOQGAEILVRGVSVKISCKGSGYFTFDYGMSWVQSHAKSLEWIGLISITYGDPSY	107				
Db	1	EVQLQQSGPELVKPGASVRMSCKSSGYIFTDFYNMWRQSHGKSLDYGISPYSYGTGY	60				
Qy	108	NQRPKGKATMTVDKSSNTAYLELARLTSEDAIYVCARS DNGTYGVYYALDYWGOGTTVTV	167				
Db	61	NQRPKGKATUTVDKSSSTAYMEURLTSEDAIVYICAGSGN---KWMDYWGHGASVTV	117				
Qy	168	SSGGSGSGGGSGGGSDIELTQSPSLAVSLGORATISCRASES-VDSYGDSPFMHWQQ	226				
Db	118	SSGGSGSGGGSGGGSDIVLTQSPASLAVSLGORATISCRSSOSLVHSGNTVLYNWYQQ	177				
Qy	227	KPGOPPKLLIYRASNLBESGPVPARFSGSGSESDFTLITDPVEEDAAVVYICLQSMEDPYTF	286				
Db	178	KPGOPPKLLIYKVSNRFSGVVPARFSGSGSESDFTLITDPVEEDAAIYVCSQTTHVPTPF	237				
Qy	287	GGGTKLEIKRAA	298				
Db	238	GSGETLELKRAA	249				

RESULT 2
US-08-894-922A-10
; Sequence 10, Application US/08894922A
; Patent No. 5863765
; GENERAL INFORMATION:
; APPLICANT: BERRY, Mark John
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOGT, Cornelius P.E.
; APPLICANT: WHITELAM, Garry Clark
; TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY

	Query Match	54.9%; Score 946.5; DB 2; Length 271;
	Best Local Similarity	70.6%; Pred. No. 4.6e-60;
	Matches 192; Conservative	20; Mismatches 39; Indels 21; Gaps 4

Qy	41	AAPAMAEVKIQSGAELVPGVSVKISCKGSGYTFTDYGMSWKQSHAKSELMIGLIST	100
Dd	16	AAQPAMAQVLQQSGAELVPKGSFKUSKASDYTFYSYWHWVKRPPQGQLWEIENP	75
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Qy	101	VYGDPSTNORFKGKATMTVDKSSNTAYLELARTLSDESAIYYCARSDGNYGYYALDYM	160
Dd	76	TNGRTTYNERPKSKATLTVDKSSSTA YMQLSLTSDESAVIYCARRYGN-----SFDYMG	130
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Qy	161	QGTTVTVSSGGGSGGGGGGGGGDIETQSPLSLAVSLGORATI SCRASESVDSYGDSF	220
Dd	131	QGTTVTVS-----SRMDKRDIETQSPLSLAVSLGORATISCRASESVDSYGNSF	180
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Qy	221	MHWYOQRFGOPKKLIIRASNLESGBPARGSGESSEDFTLTIDPVREDDAAVVYCLQSM	280
Dd	181	QMWOYQRPGPPOKKLIIRASNLESGBIPARFSGTGRITDTFLTINPVEADDVATTCQOSD	240
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Qy	281	EDP--YTFGGTGTKLEIKRAAASGGGGSGGGG 310	
Dd	241	EYPMYTFFGGTGKLEIKR---GSGSGNSGKG 268	
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RESULT 3

```

US-09-419-788-30
; Sequence 30, Application US/09419788
; Patent No. 6825325
; GENERAL INFORMATION:
; APPLICANT: FISCHER, Rainer
; APPLICANT: SCHILLBERG, Stefan
; APPLICANT: NAHRING, Jorg
; APPLICANT: SACK, Markus
; APPLICANT: MONECKE, Michael
; APPLICANT: LIAO, Yu-Cai
; APPLICANT: SPIEGEL, Holger
; APPLICANT: ZIMMERMAN, Sabine
; APPLICANT: EMANS, Neil
; TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
; FILE REFERENCE: 0147-0189p
; CURRENT APPLICATION NUMBER: US/09/419,788
; EARLY FILING DATE: 1999-10-18
; EARLY APPLICATION NUMBER: 98 11 9630.6 EP
; EARLY FILING DATE: 1998-10-16
; EARLY APPLICATION NUMBER: 66/BOM/1998 INDIA
; EARLY FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 30
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
; OTHER INFORMATION: natural origin
US-09-419-788-30

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	Query Match	53.5%	Score 923;	DB 4;	Length 267;
	Best Local Similarity	71.7%;	Pred. No. 2.1e-58;		
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Qy	48	EVKLQSGAELVRPGVSVKISKCGSYFTFDYGMWVKQSHAKSLEWTGLITYYGDSY	107		
Dd	1	EVKLQSGAELVRPGASVKISKASDYSFTGYNNWVKQSHGKSLEWIGNINPYVGTSY	60		
Qy	108	NOREPKGATMTVDKSSNTAYLEIARLTSEDSAIYYCARSDGNYYVALDYWGQTTVTV	167		
Dd	61	NQPKGKATLTVDKSSSTAYNQLNSLTSEDSAVTYCA-VGGNYVDWFA--YWGQTTLVTV	117		
Ov	168	SSGGGGGGGGGGGGDIETQSPSSLVASLGORATISCRASES-VDSYGDSFMHWYQQ	226		

APPLICANT: Iverson, Brent L.
APPLICANT: Georgiou, George
APPLICANT: Burks, Elizabeth A.
TITLE OF INVENTION: IN VITRO SCANNING SATURATION MUTAGENESIS
TITLE OF INVENTION: OF PROTEINS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,408
FILING DATE: Concurrently Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/045,409
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UT8:593
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/447-7577
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-070-408-132

Query Match 53.0%; Score 914; DB 3; Length 269;
Best Local Similarity 70.6%; Pred. No. 9.4e-58;
Matches 178; Conservative 30; Mismatches 40; Indels 4; Gaps 2;
QY 48 EVKLQSGAELVRPGVSVKISCKGSGYFTFDYGMVWKQSHAKSLEWIGLISYVGDPSY 107
DB 2 EVQLQSGPPELVRPGASVRMSCKSGYFTFDYVWVRQSHGKSLDIYGISYSGVTGY 61
QY 108 NQRFKQKATLVDKSSNTAYLELRLTSDSAIYYCARSDGNYYGYALDYWGQGTITVTV 167
DB 62 NQRFKQKATLVDKSSNTAYLELRLTSDSAIYYCARSDGN--KWAMDYWGHGASVTV 118
QY 168 SSGGGSGGGSGGGSGGSDIELTQSPSSLAVSLGORATISCRASES-VDSYGDSPFMHWYQ 226
DB 119 SSGGGSGGGSGGGSGGSDIVLTQTPPLPSVSLGDAQATISCRSSQSLVHSGNTYLNWYQ 178
QY 227 KPGQPPKLLIYRASNLSESGVPARFSGSGSDFTLTIDPVEEDAAVYYCLOSMEDPYTF 286
DB 179 KAGQSPKLLIYKVNRFSGVPGARFSGSGSDFTLTIDRVEEDAAIYYCSQTHVPPTF 238
QY 287 GGGTKLEIKRAA 298
DB 239 GSGTKLEIRAS 250

RESULT 7
US-09-423-439-32
Sequence 32, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS

NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-423-439-32
Query Match 52.6%; Score 908; DB 3; Length 673;
Best Local Similarity 64.2%; Pred. No. 6.9e-57;
Matches 179; Conservative 35; Mismatches 45; Indels 20; Gaps 5;
QY 48 EVKLQSGAELVRPGVSVKISCKGSGYFTFDYGMVWKQSHAKSLEWIGLISYVGDPSY 107
DB 20 QVQLQPGAEVLKPGASVQLSCKASGYFTGYWIHWVKRPGQGLEWIGVNPSTGRSDY 79
QY 108 NQRFKQKATLVDKSSNTAYLELRLTSDSAIYYCARSDGNYYGYALDYWGQGTITVTV 167
DB 80 NEKFKQKATLVDKSSNTAYLMQLSSLTSDSAVYYCAR-ERAYGYDDAMDYWGQGTITVTV 138
QY 168 SSGGGSGGGSGGGSGGSDIELTQSPSSLAVSLGORATISCRASESV--DSYGDSPFMHWYQ 225
DB 139 SSGGGSGGGSGGGSGGSDIELSQSPSSLAVSAGEKVTMSCKSSQSLNSRTRKNYLAWYQ 198
QY 226 QKPGQPPKLLIYRASNLSESGVPARFSGSGSDFTLTIDPVEEDAAVYYCLOSMEDPY- 284
DB 199 QRPQSPKLLIYWASTRTSGVDPDRFTGSGSGTDLTITISSVQAEDLAIIYCKOS----YT 254
QY 285 --TFGGTKLEIKRAASGGSGGGSGGGSGGGSGGGGS 321
DB 255 LRTFGGTKLEIKR-----GGGGSGGGSGGGSGGGGS 283
RESULT 8
US-08-403-853-18
Sequence 18, Application US/08403853
Patent No. 5844094
GENERAL INFORMATION:
APPLICANT: HUDSON, Peter J.
APPLICANT: LAH, Maria
APPLICANT: KORRT, Alex A.
APPLICANT: IRVING, Robert A.
APPLICANT: ATWELL, John L.
APPLICANT: MALBY, Robyn L.
APPLICANT: POWER, Barbara E.
APPLICANT: COLMAN, Peter M.
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:


```
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-203-958A-4

Query Match          50.6%; Score 873; DB 4; Length 353;
Best Local Similarity 58.7%; Pred. No. 1.1e-54;
Matches 168; Conservative 45; Mismatches 67; Indels 6; Gaps 3;

QY 16 QASKILILVAMWGFCTTA----EVSTARAAQPAEAELVQLQSGAELVRPGVSVKISCKG 71
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 ETDTLALLVLLWLLVPGSTGDPYDVPDYAGAQPARSEIQLOQTGPDELVRPGASVKISCKA 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 72 SGVTFDYDGMVWQSHAKSLEWIGLISYIGDPSNQRPKGKATMTVDKSSNTAYLELA 131
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 62 SGYSFTDYIIFWVKQSHGKSLWTGNNPNYGSTYNLAKFKGKATLTVDKSSSTAYMQLN 121
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

QY 132 RLTSSEDAIYYCARSDGNYG-VYYALDYMGGTFTVSSGGGGGGGGGGSDIELTQ 190
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 122 SLTSEDAVYICVRGVYYGSSTEAPYWCQGLTVTSAGGGGGGGGGGGSDVVMITQ 181
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

QY 191 SPSSLAVSLGORATISCRASES-VDSYGDSPFMHWYQKQCPQPKLLIYRASNLGSGVPAR 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 TPLTLITITIGQPASISCKSSQLSDGKTYLNLWLQRPQCSPTRLIYLVSKLDSGVPR 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 250 FSGSGSEDTFLTIDPVEEDDAAYVYCLQSMEDPDYTFGGGTKLEIK 295
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 242 FTGSGSGDTFLKISRVEADLGIYCWQGAHPQTFFGGGTKLEIK 287
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 11
US-09-526-738A-4
; Sequence 4, Application US/09526738A
; Patent No. 6630584
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
; APPLICANT: LTD.
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336
; CURRENT APPLICATION NUMBER: US/09/526, 738A
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Humanus
US-09-526-738A-4

Query Match          49.5%; Score 853.5; DB 4; Length 258;
Best Local Similarity 65.4%; Pred. No. 1.8e-53;
Matches 166; Conservative 29; Mismatches 48; Indels 11; Gaps 3;

QY 46 MAEVKLQSGAELVRPGVSVKISCKSGYFTFDYGMVWQSHAKSLEWIGLISYIGDP 105
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 1 MAQVKLQSGAELAKPGASVMSCKTSGYFTFTSYMMWVKORPGQGLEWIGYINPTGYT 60
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

QY 106 SYNQRFKGAATMTVDKSSNTAYLELARLTSEDAIYYCARSDGNYGYYYALDYWGQTTV 165
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 61 KYNQFKDKATLTADKSSSTAYMQLSSLTNVDSAVYYCTT-----GYSY-FDYWGQTTV 114
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

QY 166 TVSSGGGGGGGGGGGGSDIELTQSPSSLAVSLGORATISCRASESVDSYGDSPFMHWYQ 225
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 115 TVSSGGGGGGGGGGGGSDIELTQSPALMSPGPKVITTCSSASSV-----NYMHWFQ 169
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

QY 226 QKPGQPKLLIYRASNLGSPARFSGSGSEDTFLTIDPVEEDDAAYVYCLQSMEDPYT 285
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 170 QKPGTSPKLIWISSTNLASGVPARFSGSGSGTSTLSRMEADAATYYCQQRSSYPYT 229
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

QY 286 FGGGTKLEIKRAAA 299
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
```

```
Db 230 FGGGTKLQIKRAAA 243

RESULT 12
US-09-526-738A-2
; Sequence 2, Application US/09526738A
; Patent No. 6630584
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
; APPLICANT: LTD.
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336
; CURRENT APPLICATION NUMBER: US/09/526, 738A
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Humanus
US-09-526-738A-2

Query Match          49.0%; Score 844.5; DB 4; Length 256;
Best Local Similarity 65.1%; Pred. No. 7.9e-53;
Matches 164; Conservative 29; Mismatches 48; Indels 11; Gaps 3;

QY 48 EYKLOQSGAELVRPGVSVKISCKSGYFTFDYGMVWQSHAKSLEWIGLISYIGDPSY 107
   : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 1 QVKLQSGAELAKPGASVMSCKTSGYFTFTSYMMWVKORPGQGLEWIGYINPTGYTY 60
   : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

QY 108 NQRFKGAATMTVDKSSNTAYLELARLTSEDAIYYCARSDGNYGYYYALDYWGQTTV 167
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 61 NQKFKDKATLTADKSSSTAYMQLSSLTNVDSAVYYCTT-----GYSY-FDYWGQTTV 114
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

QY 168 SSGGGGGGGGGGGGGSDIELTQSPSSLAVSLGORATISCRASESVDSYGDSPFMHWYQOK 227
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 115 SSGGGGGGGGGGGGGSDIELTQSPALMSPGPKVITTCSSASSV-----NYMHWFQOK 169
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

QY 228 PQOPPKLLIYRASNLGSPARFSGSGSEDTFLTIDPVEEDDAAYVYCLQSMEDPYTFG 287
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 170 PGTSPKLIWISSTNLASGVPARFSGSGSGTSTLSRMEADAATYYCQQRSSYPYT 229
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

QY 288 GGTGLEIKRAAA 299
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 230 GGTGLEIKRAAA 241
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 13
US-08-553-497A-20
; Sequence 20, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTERBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSLOW, DETLEF
; APPLICANT: ADAN, JAUME
; APPLICANT: MITJANS, FRANCES
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCES
; APPLICANT: PIULATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESSES:
; ADDRESS: MILLER, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; MEDIUM TYPE: Floppy disk
```


COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/553,497A
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-20

Query Match 48.8%; Score 842; DB 2; Length 244;
Best Local Similarity 65.3%; Pred. No. 1.1e-52;
Matches 164; Conservative 32; Mismatches 45; Indels 10; Gaps 4;

QY 48 EVKLOQSGAELVRPGSVKISKGSGYFTDYGMSVWKSHAKSLEWIGLSTYYGDPST 107
DB 1 EVQLQSGAELVKPGASVKLSCKASGYFTTSHMMHWKQAGGLEWIGFNPNGRTNY 60

QY 108 NORFKGKATMTVDKSSNTAYLELRLTSDSAIYYCARSDGNY-GYYALDYWGQTTVT 166
DB 61 NFKFSKATLTVDKSSNTAYMQLSLTSDSAIYYCASRDYDGRYF--DYWGQTTVT 118

QY 167 VSSGGSGGGGGGGGGGGDIETQSPSLAVSLGQRATISCRASESDVSGSPFHWYQO 226
DB 119 VSSGGSGGGGGGGGGGGDIETQSPSLAVSLGQRATISCRASESDVSGSPFHWYQO 173

QY 227 KFGQPPKLLIYRASNLGSGVPARFSGSGSGSDFTLTIDPVEEDAAVYYCLOSMEDP--Y 284
DB 174 KFGSSPLLIYDTSNLASGVPVRFSGSGSGTSTSLTISRMEADAATYYCQWSSYP 233

QY 285 TFGGGTKLEIK 295
DB 234 TFGGGTKLEIK 244

RESULT 14
US-08-553-497A-18
Sequence 18, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTLEBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSOW, DETLEF
APPLICANT: ADAN, JAUME
APPLICANT: MITJANS, FRANCES
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCES
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-18

Query Match 48.6%; Score 837.5; DB 2; Length 239;
Best Local Similarity 66.1%; Pred. No. 2.3e-52;
Matches 164; Conservative 34; Mismatches 35; Indels 15; Gaps 4;

QY 48 EVKLOQSGAELVRPGSVKISKGSGYFTDYGMSVWKSHAKSLEWIGLST----YY 102
DB 1 EVKLOESGDLVKPGSLKLSAASGFTFSSYCMWVRQTPDKRLSVATISSGGAYIV 60

QY 103 GDSYNQRFGKATMTVDKSSNTAYLELRLTSDSAIYYCARSD-GNYGYYYALDYWGQ 161
DB 61 PD-----SVKGRFTTISRDNAGNTLYLQMSLSKSEDTAMYYCARLETGD----YALDYWGQ 111

QY 162 GTTAVTSSGGGGGGGGGGGGDIETQSPSLAVSLGQRATISCRASESDVSGDSFM 221
DB 112 GTTAVTSSGGGGGGGGGGGGDIETQSPSLAVSLGQRATIFCKDSQSDVDYDGSYM 171

QY 222 HWYQKPGQPPKLLIYRASNLGSGVPARFSGSGSGSDFTLTIDPVEEDAAVYYCLOSM 281
DB 172 HWYQKPGQPPKLLIYRASNLGSGVPARFSGSGSGTDFSLNIHPVEEDDIAMFYCQO 231

QY 282 DPTTFGGG 289
DB 232 VPSFGG 239

RESULT 15
US-09-423-439-51
Sequence 51, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
APPLICANT: BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS

```

;
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-NO. 6339070-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
;
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 666 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-423-439-51

Query Match      48.5%; Score 836.5; DB 3; Length 666;
Best Local Similarity 60.9%; Pred. No. 8.4e-52;
Matches 167; Conservative 26; Mismatches 64; Indels 17; Gaps 3;

QY 48 EVKLOQSGAELVRPGVSVKISKCGSGYTFDYGMVSWVKQSHAKSLEWIGLISYYGDPSPY 107
DB 20 EVQLQSGAELVRSASVKLSCTASGTFNIKDNMTMHVVKQRPQGLEWIAWIDPENGDTVEY 79
QY 108 NORFKGKATMTVDKSNNTAYLELRLTSEDSALYYCARSDGNYYGYVALDYWGQGTITVTV 167
DB 80 APKFRGKATLTADSSNTAYLHLSSLTSEDTAVYYCHVL--IYAGYLAMDYWGQGTISVAV 137
QY 168 SSGGGSGGGSGGGSGGSDIELTQSPSSLAVALGQRATISCRASESVDSYGDSPMHVYQOK 227
DB 138 SSGGGSGGGSGGGSGGSGQIVLTQSPAIMSASPGKVTITCSASSV-----TYMHWFPQK 192
QY 228 PGQPPKLLIYRASNLESGVPAFPSSGSGSDFTLTIDPVEEDDAVYYCLQSMEDPYTFG 287
DB 193 PGTSPKLIWYSTNLASGVPAFPSSGSGGTSYSLTISRMEADAATYYCQQRSTYPLTFG 252
QY 288 GGTLEIKRAAASGGGGSGGGSGGGSGGGSGGGGS 321
DB 253 AGTKLEIKR-----GGGGSGGGSGGGGS 276

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Search completed: August 23, 2005, 11:29:18
Job time : 319 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 11:29:22 ; Search time 1836 Seconds
(without alignments)
70.170 Million cell updates/sec

Title: US-10-089-278-6

Perfect score: 1725

Sequence: 1 MDCLTLNLRAGKVDQASKI.....GSGGGGSGGGGASPVQFI 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	978	56.7	260	10	US-09-782-671B-2
3	978	56.7	260	11	US-09-813-444-2
4	957	55.5	762	20	US-11-035-599-28
5	947.5	54.9	252	14	US-10-169-351-49
6	935.5	54.2	239	9	US-09-808-037-6
7	935.5	54.2	239	14	US-10-162-889-6
8	935.5	54.2	239	15	US-10-384-788-6
9	935.5	54.2	239	15	US-10-618-856-6
10	935.5	54.2	239	17	US-10-749-522-6
11	935.5	54.2	239	20	US-11-073-526-6

12	932.5	54.1	248	17	US-10-879-994-14	Sequence 14, Appl
13	932.5	54.1	248	17	US-10-610-452-14	Sequence 14, Appl
14	927	53.7	261	16	US-10-689-006-24	Sequence 24, Appl
15	918	53.2	895	16	US-10-296-085A-19	Sequence 19, Appl
16	918	53.2	895	16	US-10-296-085A-20	Sequence 20, Appl
17	918	53.2	895	16	US-10-296-085A-27	Sequence 27, Appl
18	918	53.2	895	17	US-10-496-179-4	Sequence 4, Appl
19	918	53.2	896	16	US-10-296-085A-17	Sequence 17, Appl
20	918	53.2	896	16	US-10-296-085A-18	Sequence 18, Appl
21	918	53.2	896	16	US-10-296-085A-26	Sequence 26, Appl
22	918	53.2	896	17	US-10-496-179-3	Sequence 2, Appl
23	918	53.2	896	17	US-10-496-179-7	Sequence 3, Appl
24	918	53.2	899	16	US-10-496-179-5	Sequence 7, Appl
25	918	53.2	899	16	US-10-296-085A-28	Sequence 28, Appl
26	918	53.2	899	17	US-10-496-179-5	Sequence 5, Appl
27	917.5	53.2	533	15	US-10-257-864A-96	Sequence 96, Appl
28	917.5	53.2	533	15	US-10-221-131-101	Sequence 101, App
29	917.5	53.2	533	15	US-10-399-518-125	Sequence 125, App
30	917.5	53.2	533	16	US-10-399-585-124	Sequence 124, App
31	917.5	53.2	533	16	US-10-645-085A-96	Sequence 96, Appl
32	900.5	52.2	507	15	US-10-239-656-47	Sequence 47, Appl
33	893.5	51.8	510	15	US-10-239-656-48	Sequence 48, Appl
34	893.5	51.8	510	15	US-10-239-656-49	Sequence 49, Appl
35	891.5	51.7	242	14	US-10-259-087A-18	Sequence 18, Appl
36	891.5	51.7	242	16	US-10-689-006-18	Sequence 18, Appl
37	891.5	51.7	532	20	US-11-036-098-18	Sequence 18, Appl
38	888.5	51.5	269	13	US-10-027-770-5	Sequence 5, Appl
39	887.5	51.4	264	14	US-10-114-716A-46	Sequence 46, Appl
40	887.5	51.4	264	18	US-10-930-548-46	Sequence 46, Appl
41	883.5	51.2	296	17	US-10-784-305-2	Sequence 2, Appl
42	883	51.2	274	15	US-10-257-864A-92	Sequence 92, Appl
43	883	51.2	274	16	US-10-645-085A-92	Sequence 92, Appl
44	878.5	50.9	269	13	US-10-027-770-2	Sequence 2, Appl
45	878	50.9	274	14	US-10-138-505-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-09-782-672-2
; Sequence 2, Application US/09782672
; Publication No. US2003003092A1
; GENERAL INFORMATION:
; APPLICANT: Iverson, Brent
; Chen, Gang
; Olsen, Mark J.
; Daugherty, Patrick S.
; TITLE OF INVENTION: Directed Evolution of Enzymes and
; Antibodies
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESS: ARNOLD, WHITE AND DURKEE
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,672
; FILING DATE: 12-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/847,063
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.


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Db 1 EVLQQSGPELVKPGASVRMSKSSGYIFTFDYNNWVRQSHGKSLDYIGVISPGVTGY 60
Qy 108 NORFKGKATMTVDKSSNTAYLEARLTSEDSAIYYCARSDGNYGYVALDYWGQGTITVTV 167
Db 61 NORFKGKATMTVDKSSNTAYMELRSLTSEDSAVYICAGSSGN---KWMDYWGHSVTV 117
Qy 168 SSGGGSGGGGGGGSDIELTQSPSSLAVSLGQRATISCRASES-VDSYGDSPFMHWYQQ 226
Db 118 SSGGGSGGGGGGGSDIVLTQSPASLAVSLGQRATISCRSQSLVHSGNTLYLNWYQQ 177
Qy 227 KPGQPPKLLIYRASNLSESGVPAFSGSGSESDFTLTIDPVEEDAAVYICLQSMEDPYTF 286
Db 178 KPGQPPKLLIYKVNRPFGVPAFSGSGSESDFTLTIDPVEEDAAIYYCSQTHVPPTF 237
Qy 287 GGGTKLEIKRAA 298
Db 238 GSGTKLEIKRAS 249

RESULT 4
US-11-035-599-28
; Sequence 28, Application US/11035599
; Publication No. US20050158829A1
; GENERAL INFORMATION:
; APPLICANT: Fandl, James
; APPLICANT: Chen, Gang
; APPLICANT: Papadopoulos, Nicholas
; APPLICANT: Aldrich, Thomas F.
; TITLE OF INVENTION: Fusion Polypeptides Capable of
; TITLE OF INVENTION: Activating Receptors
; FILE REFERENCE: 1080A
; CURRENT APPLICATION NUMBER: US/11/035,599
; CURRENT FILING DATE: 2005-01-14
; PRIOR FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 762
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-035-599-28

Query Match 55.5%; Score 957; DB 20; Length 762;
Best Local Similarity 72.1%; Pred. No. 1.5e-54;
Matches 186; Conservative 22; Mismatches 46; Indels 4; Gaps 1;

Qy 39 ARAAQPAEAELVKLOQSGAELVRPGVSVKISCKSGYTFDTYGMVWVKQSHAKSLEWIGLI 98
Db 24 ARGADAGAPEVKLOQSGAELMKPGASVKISCKATGYTFSGYIEWYKQRPGHGLEWIGEI 83
Qy 99 STYIGDPSYNQRFKGTATMTVDKSSNTAYLEARLTSEDSAIYYCARSDGNYGYVALDY 158
Db 84 LPSSGSGTNYNEKFKGATFTADTFSTAYWQLSSLTSEDSAVYICARFDG----YLPFDH 139
Qy 159 WGQGTITVSSGGGGGGGGGGSDIELTQSPSSLAVSLGQRATISCRASESVDSYGD 218
Db 140 WGQGTITVSSGGGGGGGGGGSDIVLTQSPASLAVSLGQRATISCRASKSVITSGY 199
Qy 219 SFMHWYQKPGQPPKLLIYRASNLSESGVPAFSGSGSESDFTLTIDPVEEDAAVYICLQ 278
Db 200 SYMHWYQKPGQPPKLLIYASNLSESGVPAFSGSGSGTDTLTNIHPVEEDAAIYYCHH 259
Qy 279 SMEDPYTFGGTKLEIKR 296
Db 260 SRELPTFGGTKLEIKR 277

RESULT 5
US-10-169-351-49
; Sequence 49, Application US/10169351
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; Publication No. US20030157090A1
; GENERAL INFORMATION:
; APPLICANT: BENVENUTO, EUGENIO
; APPLICANT: FRANCONI, ROSELLA
; APPLICANT: DESIDERIO, ANGIOLA
; APPLICANT: TAVLADORAKI, PARASKEVI
; TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES
; TITLE OF INVENTION: WHICH INCLUDE THEM
; FILE REFERENCE: 4161-4
; CURRENT APPLICATION NUMBER: US/10/169,351
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/IT00/00554
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: IT RM99A000803
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv(F8)
; OTHER INFORMATION: amino acid sequence
US-10-169-351-49

Query Match 54.9%; Score 947.5; DB 14; Length 252;
Best Local Similarity 71.1%; Pred. No. 2.1e-54;
Matches 180; Conservative 29; Mismatches 39; Indels 5; Gaps 2;

Qy 48 EVKLQSGAELVRPGVSVKISCKSGYTFDTYGMVWVKQSHAKSLEWIGLIITYYGDPSY 107
Db 1 QVQLQESGGDLVQPGGSLKSLCAASGFTFTSSYGMVWVROTDPDKRLVATINSNGSTFY 60
Qy 108 NORFKGKATMTVDKSSNTAYLEARLTSEDSAIYYCARSDGNYGYVA----LDYWGQGT 163
Db 61 PDSVKGRFTISRDNKNTLYLQWSSLKSEDTAMYICARR-RNYPYYGSRGYFDYWGQGT 119
Qy 164 TVTVSSGGGGGGGGGGSDIELTQSPSSLAVSLGQRATISCRASESVDSYGDSPFMHW 223
Db 120 TVTVSSGGGGGGGGGGSDIELTQSPASLAVSLGQRATISCRASESVDSYGNFPMHW 179
Qy 224 YQKPGQPPKLLIYRASNLSESGVPAFSGSGSESDFTLTIDPVEEDAAVYICLQSMEDP 283
Db 180 YQKPGQPPKLLIYRALNLESGIPARFSGSGSRTDFTLTINPVEADDAVYICQSNEDP 239
Qy 284 YTFGGTKLEIKR 296
Db 240 WTFGGTKLEIKR 252

RESULT 6
US-09-808-037-6
; Sequence 6, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eilat
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
; FILE REFERENCE: SOLOMON-2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 239
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; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 248
; TYPE: PRT
; ORGANISM: mus musculus
US-10-879-994-14

RESULT 12
US-10-879-994-14
; Sequence 14, Application US/10879994
; Publication No. US20050032175A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Yancopoulos, George D.
; APPLICANT: Karow, Margaret
; APPLICANT: Smith, Eric
; TITLE OF INVENTION: HIGH AFFINITY FUSION PROTEINS AND THERAPEUTIC AND DIAGNOSTIC METHODS
; FILE REFERENCE: REG 203E2
; CURRENT APPLICATION NUMBER: US/10/879,994
; CURRENT FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: 10/610,452
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 248
; TYPE: PRT
; ORGANISM: mus musculus
US-10-879-994-14

Query Match      54.1%; Score 932.5; DB 17; Length 248;
Best Local Similarity 72.0%; Pred. No. 2e-53;
Matches 180; Conservative 26; Mismatches 41; Indels 3; Gaps 2;

QY 48 EVKLQSGAELVRPGVSVKISCKSGYTTDYGMVSKQSHAKSLEWIGLSTYYGDPYS 107
Db 1 QVQLQSGAELAKPGASVSKSCASGYTFTSYMMHWIKQRPQGLGWIGVNPSTGYTEY 60
||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
QY 108 NORFKGKATMTVDKSSNTAYLELRLTSEDSAIYYCARSDGNYGYYYALDYWGQGTVTY 167
Db 61 NQKFQDKATLTADKSSSTAYMQLSSLTSEDSAVYYCARD--YYDYEDVMDYWGQGTSVNV 118
||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
QY 168 SS--GGGGGGGGGGGGSDIELTQSPSSLAIVSLGORATISCRASESVDSYGFDMHWYQQ 226
Db 119 SSAGGGGGGGGGGGSDIVLTQSPASLAIVSLGORATISCRASESVDFGIFSMNWFOQ 178
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QY 227 KPGQPPKLLIYRASNLSEGVPAFSGSGSDFTLTIDPVEEDDAAYVYCLQSMEDPYTF 286
Db 179 KPGQPPKLLIYAASNQSGVPAFSGSGSDFTSLNIHPMEEGDAAMYFCQIQKEVPWTF 238
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Query Match      54.1%; Score 932.5; DB 17; Length 248;
Best Local Similarity 72.0%; Pred. No. 2e-53;
Matches 180; Conservative 26; Mismatches 41; Indels 3; Gaps 2;

QY 48 EVKLQSGAELVRPGVSVKISCKSGYTTDYGMVSKQSHAKSLEWIGLSTYYGDPYS 107
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QY 108 NORFKGKATMTVDKSSNTAYLELRLTSEDSAIYYCARSDGNYGYYYALDYWGQGTVTY 167
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QY 168 SS--GGGGGGGGGGGGSDIELTQSPSSLAIVSLGORATISCRASESVDSYGFDMHWYQQ 226
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Query Match      54.1%; Score 927; DB 16; Length 261;
Best Local Similarity 70.1%; Pred. No. 4.8e-53;
Matches 178; Conservative 23; Mismatches 45; Indels 8; Gaps 2;

QY 46 MAEVKLQSGAELVRPGVSVKISCKSGYTTDYGMVSKQSHAKSLEWIGLSTYYGDP 105
Db 1 MAQVKLQSGPELVKPGASVSKSCASGYTFTSYMMHWIKQSHAKSLEWIGLTDYPGGT 60
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QY 106 SYNQRFKATMTVDKSSNTAYLELRLTSEDSAIYYCARSDGNYGYYYALDYWGQGT 165
Db 61 SYNQFPGKATLTVDKSSNTAYLQLKSLTSEDSAVYYCARD--GYGGFSYWGQGT 117
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QY 166 TVSSGGGGGGGGGGSDIELTQSPSSLAIVSLGORATISCRASESVDSYGFDMHWYQ 225
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; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 248
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-610-452-14

Query Match      54.1%; Score 932.5; DB 17; Length 248;
Best Local Similarity 72.0%; Pred. No. 2e-53;
Matches 180; Conservative 26; Mismatches 41; Indels 3; Gaps 2;

QY 48 EVKLQSGAELVRPGVSVKISCKSGYTTDYGMVSKQSHAKSLEWIGLSTYYGDPYS 107
Db 1 QVQLQSGAELAKPGASVSKSCASGYTFTSYMMHWIKQRPQGLGWIGVNPSTGYTEY 60
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QY 108 NORFKGKATMTVDKSSNTAYLELRLTSEDSAIYYCARSDGNYGYYYALDYWGQGTVTY 167
Db 61 NQKFQDKATLTADKSSSTAYMQLSSLTSEDSAVYYCARD--YYDYEDVMDYWGQGTSVNV 118
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QY 168 SS--GGGGGGGGGGGGSDIELTQSPSSLAIVSLGORATISCRASESVDSYGFDMHWYQQ 226
Db 119 SSAGGGGGGGGGGGSDIVLTQSPASLAIVSLGORATISCRASESVDFGIFSMNWFOQ 178
||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
QY 227 KPGQPPKLLIYRASNLSEGVPAFSGSGSDFTLTIDPVEEDDAAYVYCLQSMEDPYTF 286
Db 179 KPGQPPKLLIYAASNQSGVPAFSGSGSDFTSLNIHPMEEGDAAMYFCQIQKEVPWTF 238
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Query Match      53.7%; Score 927; DB 16; Length 261;
Best Local Similarity 70.1%; Pred. No. 4.8e-53;
Matches 178; Conservative 23; Mismatches 45; Indels 8; Gaps 2;

QY 46 MAEVKLQSGAELVRPGVSVKISCKSGYTTDYGMVSKQSHAKSLEWIGLSTYYGDP 105
Db 1 MAQVKLQSGPELVKPGASVSKSCASGYTFTSYMMHWIKQSHAKSLEWIGLTDYPGGT 60
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QY 106 SYNQRFKATMTVDKSSNTAYLELRLTSEDSAIYYCARSDGNYGYYYALDYWGQGT 165
Db 61 SYNQFPGKATLTVDKSSNTAYLQLKSLTSEDSAVYYCARD--GYGGFSYWGQGT 117
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QY 166 TVSSGGGGGGGGGGSDIELTQSPSSLAIVSLGORATISCRASESVDSYGFDMHWYQ 225
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 23, 2005, 12:27:22 ; Search time 3940 Seconds

(without alignments)
4046.134 Million cell updates/sec

Title: US-10-089-278-6

Perfect score: 1725

Sequence: 1 MDCLTLNRSAEGKVDQASKI.....GSGGGGGGGGSGGASPVQFI 329

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q=/cgn2.1/USPTO.spool_p/US10089278/runat.23082005.121734.29332/app_query.fasta.1.519

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0

-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45

-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb.htg.*

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13: gb.un.*

14: gb.vi.*

RESULT 1

AX111694

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

AX111694

Sequence 1 from Patent WO0125415.

AX111694

AX111694.1 GI:13927959

synthetic construct

synthetic construct

other sequences; artificial sequences.

1

Cichutek, K. and Engelstaedter, M.

Gene transfer in human lymphocytes using retroviral scfv cell

targeting

Patent: WO 0125415-A 1 12-APR-2001;

Bundesrepublik Deutschland LET (DE)

Location/Qualifiers

1. .1030

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="scFv kodierende Sequenz"

ORIGIN

Alignment Scores:

Pred. No.: 8.44e-118 Length: 1030

Score: 1725.00 Matches: 329

Percent Similarity: 100.00% Conservative: 0

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1725	100.0	1030	6 AX111694	AX111694 Sequence
2	1239	71.8	990	6 AX111696	AX111696 Sequence
3	1202.5	69.7	946	6 AX111697	AX111697 Sequence
4	1186.5	68.8	927	6 AX111695	AX111695 Sequence

Best Local Similarity: 100.00%		Mismatches: 0	
Query Match: 100.00%		Indels: 0	
DB: 6		Gaps: 0	
US-10-089-278-6 (1-329) x AX111696 (1-1030)			
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QY	21	LeuIleLeuValAlaTrpTrpGlyPheGlyThrAlaGluValSerThrAlaArg 40	
DB	104	CTAAATCTCTCTGGCTTGGTGGGGTTGGGACCACTGCCGAAGTTCCGACTGCCGA 163	
QY	41	AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerClyAlaGluLeuValArg 60	
DB	164	GCGGCCACCGCCCATATGCGGAGGTCAGCTGCAGAGTCAGCGGCTGAGCTGGGAGG 223	
QY	61	ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80	
DB	224	CTGGGGTCTCAGTGAAGATTCTCGAAGGTTCTGGCTACACATTCAGTATATGGT 283	
QY	81	MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100	
DB	284	ATGAGCTGGTGAAACAGAGTCATGCAAGAGTCTAGAGTGGATTGGACTTATTAGTACT 343	
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DB	344	TACTATGGTGATCCTAGTTACACACAGAGGTTCAAGGGCAAGCCCAATGACTGTAGAC 403	
QY	121	LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140	
DB	404	AAATCTCCACACAGCCTATTGGAACTTGCAGACTGCAGACTGCAGGATCTGCCATT 463	
QY	141	TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGly 160	
DB	464	TATTATTGTGCAAGATCGGATGTAATTACGGGTATTACTATGCTTTGGACTACTGGGC 523	
QY	161	GlnGlyThrValThrValSerSerGlyGlyGlySerGlyGlyGlyGlySerGly 180	
DB	524	CAAGGCACATACGGTCCCGTCTCCTCAGGTGGAGGGGTTGAGCGGAGGTGGCTCTGGC 583	
QY	181	GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200	
DB	584	GGTGGCGGATCGATATCGAGCTCACTCAGTCTCCATCTTCTTGGCTGTCTCTAGGG 643	
QY	201	GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220	
DB	644	CAGAGGGCCACCATATCTCTGCAGAGCAGTGAAGTGTGATAGTTATGGCGATAGTTT 703	
QY	221	MetHisTrpTrpGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSer 240	
DB	704	ATGCATGGTATCAGCAGAAACAGGACAGCCACCACTCTCATCTATCTGTGATCC 763	
QY	241	AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260	
DB	764	AACTAGATCTGAGTCCCTCGCAGGTTCAGTGGCAGTGGCTCTGAGTCAGACTTCACT 823	
QY	261	LeuThrIleAspProValGluGluAspAlaValTyrTyrCysLeuGlnSerMet 280	
DB	824	CTCACCATCATCTGTGGAGGAAGATGATGCTGCAGTGATTTACTGTCTGCAAAATG 883	
QY	281	GluAspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAlaSer 300	
DB	884	GAGATCCGTACAGTTTCGGAGGGGGACCAAGCTGGAAATAAACAAGGGCGGCATCG 943	
QY	301	GlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly 320	
DB	944	GGCTCCGGGGCGGTGGTCTGGTGGTGTCTGGTGGTGGTGGTGGTGGTGGTGGT 1003	
QY	321	SerGlyAlaSerProValGlnPheIle 329	
DB	1004	TCCTGGGCCAGCCAGTCCAGTTTATC 1030	

RESULT 2

AX111696

LOCUS

AX111696 Sequence 3 from Patent WO0125415. 990 bp DNA linear PAT 30-APR-2001

DEFINITION

AX111696

ACCESSION

AX111696

VERSION

AX111696.1 GI:13927961

KEYWORDS

SOURCE

ORGANISM

synthetic construct

other sequences; artificial sequences.

REFERENCE

1

AUTHORS

Cichutek,K. and Engelstaedter,M.

TITLE

Gene transfer in human lymphocytes using retroviral scfv cell

JOURNAL

targeting

Patent: WO 0125415-A 3 12-APR-2001;

Bundesrepublik Deutschland LET (DE)

FEATURES

Location/Qualifiers

1..990

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="scfv kodierende Sequenz"

ORIGIN

Alignment Scores:

Pred. No.: 3.96e-82 Length: 990

Score: 1239.00 Matches: 243

Percent Similarity: 82.23% Conservative: 30

Best Local Similarity: 73.19% Mismatches: 45

Query Match: 71.83% Indels: 14

DB: 6 Gaps: 5

US-10-089-278-6 (1-329) x AX111696 (1-990)

QY

1

MetAspCysLeuThrAsnLeuArgSerAlaGluGlyValAspGlnAlaSerLysIle 20

DB

1

ATGGACTGTCACCAACCTCCGATCCGCTGAGGTAAGTTGACCGAGCGCAAAATC 60

QY

21

LeuIleLeuValAlaTrpTrpGlyPheGlyThrAlaGluValSerThrAlaArg 40

DB

61

CTAAATCTCTCTGGCTTGGTGGGGTTGGGACCACTGCCGAAGTTTCGACTGCCGA 120

QY

41

AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg 60

DB

121

GCGGCCACCGCCCATATGCGGAGGTCAGCTGCAGACTGCACTGGAACCTGGAACA 180

QY

61

ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80

DB

181

CCTGGGGCCTCAGTGAAGATGCTCTGCAAGGCTTCTGGCTACGCCCTTTACTACTACTGG 240

QY

81

MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIle----- 98

DB

241

ATGCATGGTGAACAGAGGCTGCAGAGGCTCGAATGGATTGGATATCATTAATCCT 300

QY

99

SerThrTyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThr 118

DB

301

ACCACCTGATTATCTGAC-----TACAATCTCAAGTTCAAGGACAAGGCCACATTGACT 354

QY

119

ValAspLysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSer 138

DB

355

GCAGACAAATCTCTCCAGTACAGCCTACATGCAACTGAGCAGCCTGCATCTGAGGACTCT 414

QY

139

AlaIleTyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyr 158

DB

415

GCAGCTTATTACTGTGCAAGATCG-----GGGTGGTCTCTATGCTATGGACTAC 462

QY

159

TrpGlyGlnGlyThrThrValThrValSerSerGlyGlyGlyGlySerGlyGlyGly 178

DB

463

TGGGGGCAAGGGACCAAGCTCACCATCTCTCAGGTGGAGGCGGTTTCAGCGGAGGTGC 522

QY

179

SerGlyGlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSer 198

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Db      523  TCTGGCGGTGGCGGATCGGACATCGAGTCACTCAGTCTCCAGCAATCATGTCTGCATCT 582
Qy      199  LeuGlyGlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyGlyAsp 218
Db      583  CCAGGGAGAGGTCACCAATAACCTGCAGTGCAGGTCACCAAGTGA----- 627
Qy      219  SerPheMetHisTrpTyGlnGlnLysProGlyGlnProProLysLeuLeuIleTyArg 238
Db      628  AGTTACATGCACTGGTTCACGAGAGACCGAGGCACTTCTCCAAACTCTGGATTTATAGC 687
Qy      239  AlaSerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAsp 258
Db      688  ACATCAACACCTGGCTTCTGAGTCCCTGCTCGTTCAGTGGCAGTGGATCTGGGACCTCT 747
Qy      259  PheThrLeuThrIleAspProValGluGluAspAlaValTyTyTyCysLeuGln 278
Db      748  TACTCTCTCAATACGACCAATGGAGGCTGAGAGTCTGCCACTTATTATCTCCAGCAA 807
Qy      279  SerMetGluAspProTyThrPheGlyGlyGlyThrLysLeuGluLeuLysArgAlaAla 298
Db      808  AGGAGTAGTTACCATTCAGTTTCGGCTCGGGACCAAGCTGGANATCAACCGGGCGGCC 867
Qy      299  AlaSerGlySerGlyGlyGlySer---GlyGlyGlySerGlyGlyGlySerGly 317
Db      868  GCATCGGGCTCCGGGGCGGTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 927
Qy      318  GlyGlyGlySerGlyAlaSerProValGlnPheIle 329
Db      928  GGTGGTGGTTCGGCGCCAGCCAGTCCAGTTTATC 963

RESULT 3
AX111697
LOCUS      AX111697              946 bp      DNA      linear      PAT 30-APR-2001
DEFINITION Sequence 4 from Patent WO0125415.
ACCESSION AX111697
VERSION    AX111697.1  GI:13927962
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Cichutek, K. and Engelstaedter, M.
TITLE      Gene transfer in human lymphocytes using retroviral scfv cell
           targeting
JOURNAL    Patent: WO 0125415-A 4 12-APR-2001;
           Bundesrepublik Deutschland LET (DE)
FEATURES   Location/Qualifiers
           source
             1..946
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="scfv kodierende Sequenz"

ORIGIN
Alignment Scores:
Pred. No.:      1.8e-79      Length:      946
Score:          1202.50      Matches:    236
Percent Similarity: 83.12%      Conservative: 30
Best Local Similarity: 73.75%      Mismatches: 47
Query Match:     69.71%      Indels:     7
DB:              6          Gaps:        4

US-10-089-278-6 (1-329) x AX111697 (1-946)

Qy      1  MetAspCysLeuThrAsnLeuArgSerAlaGluGlyLysValAspGlnAlaSerLysIle 20
Db      1  ATGGACTGTCTCACCAACCTCCGATCCGCTGAGGGTAAAGTTGACCAGCGGACAAATC 60
Qy      21  LeuIleLeuValAlaThrTrpGlyPheGlyThrAlaGluValSerThrAlaArg 40
Db      61  CTAATTCTCTTGTGGCTGGTGGGGGTTGGGACCACTGCCCAAGTTTCGACTGCCGCA 120
Qy      41  AlaAlaGlnProAlaMetAlaGluValLysLeuGlnLysSerGlyAlaGluLeuValArg 60

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Db      121  GCGGCCAGCGCGCCATGGCCGAGGTCAGCTCAGCAGCATCGGGGCTGAGCTGGTGGG 180
Qy      61  ProGlyValSerValLysIleSerCysLysGlySerGlyTyThrPheThrAspTyGly 80
Db      181  CTTGGAGCTTCAGTGAAGTGTCTCTGCAAGACTTCTGGCTTCTCTTCCACGACTACTGG 240
Qy      81  MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
Db      241  ATGAACCTGGGTGAAGCTGAGCCCTGGACAAGGCTTGAAGTGGATTTGGCATGATTCATCCT 300
Qy      101  TyTyTyGlyAspProSerTyAsnGlnAtrgPheLysGlyLysAlaThrMetThrValAsp 120
Db      301  TCCGATAGTGAACACTAGTTAACTCAGAGGTTCAAGGACAAGCCACACTGACTGTAGAC 360
Qy      121  LysSerSerAsnThrAlaTyLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db      361  AATCTCTCCAGCACAGCTACATGCAACTCAGCAGCCGACATCTGAGGACTCTGCGGTC 420
Qy      141  TyTyTyCysAlaArgSer---AspGlyAsnTyGlyTyTyTyTyAlaLeuAspTyTyTrp 159
Db      421  TATTACTGTGCAAGATCTCTTTATGCTAACTACCCCTCTGGTTTACT-----TACTGG 474
Qy      160  GlyGlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlyGlySer 179
Db      475  GGCCAGGACCAACGCTCAGCTCTCTCAGGTGGAGCGGTTCAGGCGAGGTGGTCTCT 534
Qy      180  GlyGlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeu 199
Db      535  GCGGTGGCGGATCGGACATCGAGTCACTCAGTCTCCAACCACTGCTGCTGCTGCTCCC 594
Qy      200  GlyGlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyGlyAspSer 219
Db      595  GGGGAGAAATCACTATCACTCAGTGCAGTCCAGCTCAAGTATATAAGTTTCC-----AAT 645
Qy      220  PheMetHisTrpTyGlnGlnLysProGlyGlnProProLysLeuLeuIleTyArgAla 239
Db      646  TACTTGCATTTGGTATCAGCAGAACCGAGATTTCCCTTAACCTTGTATTATAGGACA 705
Qy      240  SerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPhe 259
Db      706  TCCAATCTGGCTTCTGGAGTCCAGCTCGCTTCACTGGCAGTGGTCTGGGACCTCTTAC 765
Qy      260  ThrLeuThrIleAspProValGluGluAspAlaAlaValTyTyTyCysLeuGlnSer 279
Db      766  TCTCTCACAATTGGCCACCATGGAGGCTGAAGATGTTGCCACTTACTTCTGCCAGCGGT 825
Qy      280  MetGluAspProTyThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAlaAla 299
Db      826  AGTAGTATACCGTACACGTTCCGAGGGGGGAGCCACAGCTGGAAATAAAGCGGGCGCGCA 885
Qy      300  SerGlySerGlyGlyGlyGlySer---GlyGlyGlySerGlyGlyGlySerGlyGly 318
Db      886  TCGGGCTCCGGGGCGGTGTTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 945

RESULT 4
AX111695
LOCUS      AX111695              927 bp      DNA      linear      PAT 30-APR-2001
DEFINITION Sequence 2 from Patent WO0125415.
ACCESSION AX111695
VERSION    AX111695.1  GI:13927960
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Cichutek, K. and Engelstaedter, M.
TITLE      Gene transfer in human lymphocytes using retroviral scfv cell
           targeting
JOURNAL    Patent: WO 0125415-A 2 12-APR-2001;
           Bundesrepublik Deutschland LET (DE)
FEATURES   Location/Qualifiers
           source
             1..927

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="ScFv kodierende Sequenz"

ORIGIN

Alignment Scores:

Pred. No.: 2,63e-78 Length: 927
Score: 1186.50 Matches: 229
Percent Similarity: 79.69% Conservative: 26
Best Local Similarity: 71.56% Mismatches: 54
Query Match: 68.78% Indels: 11
DB: 6 Gaps: 2

US-10-089-278-6 (1-329) x AX111695 (1-927)

QY 1 MetAspCysLeuThrAsnLeuArgSerAlaGluGlyValAspGlnAlaSerLysIle 20
DB 1 ATGGACTGTCTCAACCACTCCGATCCGCTGAGGTAAGTTACACAGCGCAGCAAAATC 60
QY 21 LeuIleLeuValAlaTTPtGlyPheGlyThrThraAlaGluValSerThrAlaArg 40
DB 61 CTAATTTCTCTGTGGCTTGGTGGGGTTGGGACCACTGCCAAGTTTCGACTGCCCGA 120
QY 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg 60
DB 121 GCGGCCAGCGCCATGGCGAGGTCAGCTCAGAGTCAGGACTGNACTTGTGAAG 180
QY 61 ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
DB 181 CCTGGGGTTCAGTGAATCTCTTGCAGGCTCTGGCTACACCTTACCAGCTACTGG 240
QY 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
DB 241 ATGCACCTGGTGAAGCAGAGCGCTCGACCAAGCGCTTGAGTGGATCGAGAGATTGATCCT 300
QY 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
DB 301 GTTGATAGTTATCTACTACATCAAACTTCAGGGCAGGCCACACACTGACTGTAGAC 360
QY 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
DB 361 AAGTCTCTCCACACAGCTACATGCACCTCAGCAGCGCTGACATCTGAGGACTCTGGCGTC 420
QY 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrAlaLeuAspTyrTrpGly 160
DB 421 TATTACTGTGCAGAAAGGCG-----TATGCTATGGACTACTGGGCG 462
QY 161 GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 180
DB 463 CAAGGACCAACCTCACCGTCTCTCAGGTGGATGCGGTTTCAGCGGAGGTGGCTCTGGC 522
QY 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200
DB 523 GGTGGCGGATCGGACATCGAGCTCACTCAGTCCACGCAATCATGTCTGCACTCTCCAGGG 582
QY 201 GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220
DB 583 GAGAAGGTCAACAGTACCTCGATGTCAGCTCAAGTATA-----AGTTAC 627
QY 221 MetHisTrpTyrGlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArgAlaSer 240
DB 628 ATGCACCTGGTACCAGCAGAGCCAGGCACCTCCCCCAAAAGATGGATTATGACACATCC 687
QY 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260
DB 688 AAACCTGGCTTCTGAGTCCCTGCTCGCTTCACTGAGTGGAGTGGGCTCTGGACCTCTATTCT 747
QY 261 LeuThrIleAspProValGluGluAspAlaValTyrTyrCysLeuGlnSerMet 280
DB 748 CTCCCAATCAGCAGCAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCATCAGCGAGT 807
QY 281 GluAspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAlaSer 300

DB 808 AGTTACCCATGAGCGTTTCGTTGAGGACCAAGTGTGAAATAAAACGGCGCGCATCG 867
QY 301 GlySerGlyGlyGlySerGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGly 320
DB 868 GGCTCCGGGGCGGTGTTCTGTTGTTCTGTTGTTCTGTTGTTCTGTTGTTGTTGTT 927
RESULT 5
SYN507107 1632 bp RNA linear SYN 02-SEP-2002
LOCUS Synthetic construct for anti-CD28 and anti-HMWG ScFv antibody,
DEFINITION clone r28M.
ACCESSION AJ507107
VERSION AJ507107.1 GI:22759563
KEYWORDS antibody; heavy chain; immunoglobulin; light chain; ScFv; variable region.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Grosse-Hovest L.
TITLE Produktion und Charakterisierung supra-agonistischer bispezifischer CD28-Antikörper zur Tumor-Immuntherapie
JOURNAL Thesis (2002) Department of Biology, University of Tuebingen, Tuebingen, Germany
REFERENCE 2 (bases 1 to 1632)
AUTHORS Grosse-Hovest L.
TITLE Direct Submission
JOURNAL Submitted (28-AUG-2002) Grosse-Hovest L., Membrane Biochemistry, Max-Planck-Institute for Biochemistry, Am Klopferspitz 18a, 82152 Martinsried, GERMANY
FEATURES
Location/Qualifiers
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439..798
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/cell_line="hybridoma 9.3"
856..1218
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/mol_type="other RNA"
/db_xref="taxon:10090"
/cell_line="hybridoma 9.2.27"
1264..1599
/organism="Mus musculus"
/mol_type="other RNA"
/db_xref="taxon:10090"
/cell_line="hybridoma 9.2.27"
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/protein_id="CAD45042.1"
/db_xref="GI:22759564"


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Db 61 TCCTGCAAGGTTCTGGCTACACATTCATCATGATTAATGCTGTGCACCTGGGTGAAGCAGAGT 120
Qy 88 HisAlaLysSerLeuGluTrpLleGlyLeuLysSerThrTyrTyrGlyAspProSerTyr 107
Db 121 CATGCAAGAGTCTAGAGTGGATTGGAGTTATTAGTACTTACTATGTTGATGCTGACTAC 180
Qy 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
Db 181 AACCCGAAGTTCAAGGCAAGGCCACATTCGACTGTAACCAAGTCCCTCCAAACACAGCCAT 240
Qy 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaAaGSerAsp 147
Db 241 ATGGAACCTCCAGACTGACATCTGAGGATCTGCCATCTATTACTGTGCAAGAGGGGT 300
Qy 148 GlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrThrValThrVal 167
Db 301 AAGGGT-----GCTATGCACTATTGGGTCAGGAACCTCAGTCACCGTC 345
Qy 168 SerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlySerAspLleGlu 187
Db 346 TCC-----TCAGACATCGAG 360
Qy 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrLysSerCys 207
Db 361 CTACTCAGTCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGGCCATCATATCTCTGC 420
Qy 208 ArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTrpTyrGlnGlnLys 227
Db 421 AGAGCCAGTGAAGTGTGATAGTATGGCAATAGTTTATGCACCTGGTACACGACAGAA 480
Qy 228 ProGlyGlnProProLysLeuLeuLleTyrArgAlaSerAsnLeuGluSerGlyValPro 247
Db 481 CCAGGACAGCCACCCAACTCCTCATCTATCGTCATCCCAACCTAGAAATCTGGATCCCT 540
Qy 248 AlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrLleAspProValGlu 267
Db 541 GCCAGGTTTCAGTGGCAGTGGTCTAGGACAGACTTCACCCCTCACCATTAACTCTGTGGAG 600
Qy 268 GluAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGly 287
Db 601 GCTGATGATGTGCAACTATTACTGTACAGAAAGTAATGAGGATCCGTACACGTTCCGA 660
Qy 288 GlyGlyThrLysLeuGluLleLysArg 296
Db 661 GGGGGGACCAAGCTGGAAATAAAACGG 687

RESULT 9
AX111698 LOCUS AX111698 906 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 5 from Patent WO0125415.
ACCESSION AX111698
VERSION AX111698.1 GI:13927963
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1.
AUTHORS Gichutek,K. and Engelstaedter,M.
TITLE Gene transfer in human lymphocytes using retroviral scfv cell
targeting
JOURNAL Patent: WO 0125415-A 5 12-APR-2001;
Bundesrepublik Deutschland LfT (DE)
FEATURES
source
1. 906
/organism="synthetic construct"
/mol type="unassigned DNA"
/db xref="taxon:32630"
/note="scFv kodierende Sequenz"
ORIGIN
Alignment Scores:

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Pred. No.: 6,46e-65 Length: 906
Score: 1004.00 Matches: 196
Percent Similarity: 78.90% Conservative: 47
Best Local Similarity: 63.64% Mismatches: 51
Query Match: 58.20% Indels: 14
DB: Gaps: 4

US-10-089-278-6 (1-329) x AX111698 (1-906)

Qy 1 MetAspCysLeuThrAsnLeuArgSerAlaGluGlyLysValAspGlnAlaSerLysIle 20
Db 1 ATGGACTGTCTCAACCACTCCGATCCGCTGAGGGTAAAGTTGACCGAGCGAGCAAAATC 60
Qy 21 LeuLleLeuValAlaTrpTrpGlyPheGlyThrThrAlaGluValSerThrAlaArg 40
Db 61 CTAAATCTCTGTGTGGCTTGGTGGGGTTTGGACCACTGCCGAAAGTTTCGACTGCCGGA 120
Qy 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg 60
Db 121 CGGGCCAGCCGCCCATGGCCAGGTACAGCTGCAGAGTCAGGACGACAGAAATGAAAG 180
Qy 61 ProGlyValSerValLysLysSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
Db 181 CCGGGGAGTCTCTGAAATCTCTCTAAGGGTTTGGATACGACTTTAGCACCTACTGG 240
Qy 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpLleGlyLeuLysSerThr 100
Db 241 ATCGCTGGTGGCCAGATGCCCGGAAAGGCTGGAGTACATGGGCTCATCTATCCT 300
Qy 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db 301 GGTGACTCTGACACCAATAACACCCGCTCTCTCAAGGGCCAGGTACCATCTCAGCGGAC 360
Qy 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db 361 AAGTCATCAGCACCCCTCCTCGACGTGGAGCGCTGAAGCCCTCGGACACCGCATG 420
Qy 141 TyrTyrCysAlaArgSerAspGly-----AsnTyrGlyTyr 152
Db 421 TATTACTGTGGAGAGTCTCTGGATATTGTAGTAGTACCAGCTGTGTATGACTAC--TAC 477
Qy 153 TyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrThrValThrValSerSerGlyGlyGly 172
Db 478 TACTACTACATGACGCTCTGGGCGCGGGAACCCCTGTCACCGTCTCGAGAGGTGGAGGC 537
Qy 173 GlySerGlyGlyGlySerGlyGlyGlySerAspLleGluLeuThrGlnSerPro 192
Db 538 GGTTCAGGGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGTGATGATGCCAGTCTCCT 597
Qy 193 SerSerLeuAlaValSerLeuGlyGlnArgAlaThrLleSerCysArgAlaSerGluSer 212
Db 598 TCCACCTGTCTGCATCTCTAGGACAGACAGATCACCATGACTTGGCGGCGCAGTCAGAAC 657
Qy 213 ValAspSerTyrGlyAspSerPheMetHisTrpTyrGlnGlnLysProGlyGlnPro 232
Db 658 ATTAATATCTGG-----TTGGCCTGTATCAGCAGAAACCCAGGAAAGCCCT 705
Qy 233 LysLeuLleTyrArgAlaSerAsnLeuGluSerGlyValProAlaArgPheSerGly 252
Db 706 AAGCTCTCTGATCTATAGGGCTCCACTTCTCACCATCAGCGGCTCGAGCCGTGATGTTTGA 765
Qy 253 SerGlySerGluSerAspPheThrLeuThrLleAspProValGluGluAspAspAlaAla 272
Db 766 AGTGGATCTGGGACAGAAATTCATCTCACCATCAGCGGCTCGAGCCGTGATGATTTTGA 825
Qy 273 ValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGlyGlyThrLysLeu 292
Db 826 AGTTATTACTGT---CAACGGTATGATGACTGTGTGTGGCCCAAGGACCAAGCTG 882
Qy 293 GluLleLysArgAlaAlaLysSer 300
Db 883 GAGATCAACGTGGCGCCGATCG 906

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[illegible]

Db	166	ATGAACCTGGTGAAGCAGAGGCGCTGCACAGGGTCTTTCAGTGGATTGGACGGATTATTCCT	225	US-10-089-278-6 (1-329) x AX100194 (1-876)
Qy	101	TyTyrGlyAspProSerTyrAsnGlnArgPheLysGlyIleValThrMetThrValAsp	120	
Db	226	GGAAATGGAGATCACTACATACATGGGAAGTTCAAGGGCAAGCCACACTGACCTGCAGAC	285	
Qy	121	LysSerSerAsnThrAlaTyrLeuAlaArgLeuThrSerGluAspSerAlaIle	140	
Db	286	AAATCCTCAGCAGACGCTACATGAGCTCAGCAGGCTGACCTCTGTGACCTCTGGGGTC	345	
Qy	141	TyTyrCysAlaArgSerAspGlyAsnTyrGlyIleValThrSerGluAspSerAlaIle	160	
Db	346	TATTTCTGTGCA-----GATGTAACGTA--TATTACTATGCTATGCTACTGGGT	396	
Qy	161	GlnGlyThrValThrValSerSerGlyGlyIleValThrSerGluAspSerAlaIle	180	
Db	397	CAAGGAACCTCAGTACCGCTCTCCTCAGGTGGAGCGGTTTCAGTGGCGCGCTCTGGC	456	
Qy	181	GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly	200	
Db	457	GGTGGCGGATCGAAATGTTCTACCCAGTCTCTGCTTCTTGTATCTCTGGGG	516	
Qy	201	GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe	220	
Db	517	CAGAGGGCCACCATCTCATGCGAGGCGCCAGCAAAAGTGTCACTATCTGCTATAGTTAT	576	
Qy	221	MetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuIleValThrArgAlaSer	240	
Db	577	ATGCATCTGGTACCACAGAAACAGGACAGCCACCCAACTCTCTCATCTATCTTGGATCC	636	
Qy	241	AsnLeuGlySerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr	260	
Db	637	AACTAGATCTGGGGTCCCTGCCAGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACC	696	
Qy	261	LeuThrIleAspProValGluAspAspAlaValTyrTyrCysLeuGlnSerMet	280	
Db	697	CTCAACATCCATCTCTGTGGAGGAGGATGCTGCAACCTATTACTGTGTCAGCAGTAGG	756	
Qy	281	GluAspProTyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAla	299	
Db	757	GAGCTTCTCGGACGTTCTGGTGGAGGACCAAGCTGGAATCAACGGGGCGCGCA	813	
RESULT 13				
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LOCUS	Sequence 101 from Patent WO0119992.	876 bp	DNA	linear
DEFINITION	Sequence 101 from Patent WO0119992.			
ACCESSION	AX100194			
VERSION	AX100194.1	GI:13539109		
KEYWORDS	synthetic construct			
SOURCE	synthetic construct			
ORGANISM	other sequences; artificial sequences.			
REFERENCE	1			
AUTHORS	Scheifflinger, F., Kerschbaumer, R., Falkner, F.G. and Dörner, F.			
TITLE	Factor ix/factor ixa antibodies and antibody derivatives			
JOURNAL	Patent: WO 0119992-A 101 22-MAR-2001;			
	Baxter Aktiengesellschaft (AT)			
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Score:	992.50	Matches:	195	
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Query Match:	75.54%	Indels:	3	
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Qy	61	ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly	80	
Db	106	CCGGGGCCCTCAGTGAAGATTTCTGCAAAAGCTTCTGGCTACGCATTTCAGTAGCTCTGG	165	
Qy	81	MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr	100	
Db	166	ATGAACCTGGTGAAGCAGAGGCTGCACAGGGTCTTTCAGTGGATTGGACGGGATTATCTCT	225	
Qy	101	TyTyrGlyAspProSerTyrAsnGlnArgPheLysGlyIleValThrMetThrValAsp	120	
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Qy	121	LysSerSerAsnThrAlaTyrLeuAlaArgLeuThrSerGluAspSerAlaIle	140	
Db	286	AAATCCTCAGCAGACGCTACATGAGCTCAGCAGGCTGACCTCTGTGACCTCTGGGGTC	345	
Qy	141	TyTyrCysAlaArgSerAspGlyAsnTyrGlyIleValThrSerGluAspSerAlaIle	160	
Db	346	TATTTCTGTGCA-----GATGTAACGTA--TATTACTATGCTATGCTACTGGGT	396	
Qy	161	GlnGlyThrValThrValSerSerGlyGlyIleValThrSerGluAspSerAlaIle	180	
Db	397	CAAGGAACCTCAGTACCGCTCTCCTCAGGTGGAGCGGTTTCAGTGGCGCGCTCTGGC	456	
Qy	181	GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly	200	
Db	457	GGTGGCGGATCGAAATGTTCTACCCAGTCTCTGCTTCTTGTATCTCTGGGG	516	
Qy	201	GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe	220	
Db	517	CAGAGGGCCACCATCTCATGCGAGGCGCCAGCAAAAGTGTCACTATCTGCTATAGTTAT	576	
Qy	221	MetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuIleValThrArgAlaSer	240	
Db	577	ATGCATCTGGTACCACAGAAACAGGACAGCCACCCAACTCTCTCATCTATCTTGGATCC	636	
Qy	241	AsnLeuGlySerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr	260	
Db	637	AACTAGATCTGGGGTCCCTGCCAGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACC	696	
Qy	261	LeuThrIleAspProValGluAspAspAlaValTyrTyrCysLeuGlnSerMet	280	
Db	697	CTCAACATCCATCTCTGTGGAGGAGGATGCTGCAACCTATTACTGTGTCAGCAGTAGG	756	
Qy	281	GluAspProTyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAla	299	
Db	757	GAGCTTCTCGGACGTTCTGGTGGAGGACCAAGCTGGAATCAACGGGGCGCGCAC	816	


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/notes="scfv region"

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Alignment Scores:
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Score: 992.50 Matches: 195
Percent Similarity: 83.78% Conservative: 22
Best Local Similarity: 75.29% Mismatches: 39
Query Match: 57.54% Indels: 3
DB: 6 Gaps: 2

US-10-089-278-6 (1-329) x AX100188 (1-969)
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Db 106 CCCGGGCGCTCAGTGAAGATTTCTCGAAGCTTCTGGCTACGATTCAGTAGCTCTGG 165
QY 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
Db 166 ATGAACCTGGTGAAGCAGAGCGCTGGACAGGGTCTTGAGTGGATTCGACGGATTATCCT 225
QY 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
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QY 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
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QY 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGly 160
Db 346 TATTTCTGTGCA-----GATGTAACGTA---TATTACTATGCTATGACTACTGGGT 396
QY 161 GlnGlyThrValThrValSerSerGlyGlyGlyGlySerGlyGlyGlyGlySerGly 180
Db 397 CAAGGAACCTCAGTCACCGTCTCTCAGGTGGAGCGGTTTCAGTGGCGCGCTCTGGC 456
QY 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200
Db 457 GGTGGCGGATCGCAATTGTTCTACCCAGTCTCTGCTTCTTCTTACTGTATCTCTGGG 516
QY 201 GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220
Db 517 CAGAGGGCCACCATCTCATGCGGGCCAGCAAAAGTGTCAGTACATCTGGCTATAGTTAT 576
QY 221 MetHisTrpTyrGlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArgAlaSer 240
Db 577 ATGCACCTGTATACACAGAACACAGACAGCCACCAAACTCTCATCTATCTTGCATCC 636
QY 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260
Db 637 AACCTAGATCTGGGTCTCTGCGAGGAGGAGGATGCTGCAACCTATTACTGTCTAGCAG 696
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QY 281 GluAspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAla 299
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RESULT 14
AF003705
LOCUS
DEFINITION
partial cds.
ACCESSION
AF003705
VERSION
AF003705.1 GI:3322214

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
REMARK
COMMENT
FEATURES
source
CDS

synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 687)
Amedorfer,P., Wong,C., Chen,S., Smith,T., Deshpande,S.,
Sheridan,R., Finnern,R. and Marks,J.D.
Molecular characterization of murine humoral immune response to
botulinum neurotoxin type A binding domain as assessed by using
phage antibody libraries
Infect. Immun. 65 (9), 3743-3752 (1997)
97427959
9284147
2 (bases 1 to 687)
Amedorfer,P.
Direct Submission
Submitted (13-MAY-1997) Anesthesia, University of California at San
Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
3 (bases 1 to 687)
Amedorfer,P.
Direct Submission
Submitted (16-JUL-1998) Anesthesia, University of California at San
Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
Sequence update by submitter
On Jul 16, 1998 this sequence version replaced gi:2306924.
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Alignment Scores:
Pred. No.: 4.2e-64 Length: 687
Score: 991.00 Matches: 194
Percent Similarity: 83.53% Conservative: 14
Best Local Similarity: 77.91% Mismatches: 21
Query Match: 57.45% Indels: 20
DB: 12 Gaps: 2

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QY 68 SerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpValLysGlnSer 87
Db 61 TCTTCAAGGCTTCGGCTACACATTTCATTGATTATGCTATGCTATGCTACTGACTAC 120
QY 88 HisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107
Db 121 CTGCAAGAGCTAGAGTGGATTGGAGTTATAGTAGTTACTATGCTACTGACTACTAC 180
QY 108 AsnGlnArgPheGlyGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
Db 181 AACCAAGATCTTCAAGGGCAAGCCACATTGACTGTAGACAAATCTCTCAACACAGCTAT 240
QY 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAsp 147
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Qy      168  SerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerAspIleGlu 187
Db      346  TCC-----TCAGACATCGAG 360
Qy      188  LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
Db      361  CTCACCTCAGCTCCAGCTCTTTGGCTGTGTCTCTAGGGCAGAGGCCCATCATATCCTGC 420
Qy      208  ArgAlaSerGlnSerValAspSerTyrGlyAspSerPheMetHisTyrTyrGlnGlnLys 227
Db      421  AGAGCCAGTGAAGTGTGATAGTATGCAATAGTATTTATGCACCTGGTACCAGCAGAAA 480
Qy      228  ProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGlyValPro 247
Db      481  CCAGGACAGCCACCCAACTCCTCATCTATCGTGCACTCAACCTAGAACTGGGATCCCT 540
Qy      248  AlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspProValGlu 267
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Qy      268  GluAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGly 287
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Db      661  GCTGGGACCAAGCTGGAGCTGAACCC 687

RESULT 15
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LOCUS   CQ881538 897 bp DNA linear PAT 11-OCT-2004
DEFINITION Sequence 44 from Patent WO2004083373.
ACCESSION CQ881538
VERSION   CQ881538.1 GI:54034468
KEYWORDS .
SOURCE   Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS  Toms,G., Rutledge,E. and Mekseepalard,C.
TITLE    Antibody against the g glycoprotein of respiratory syncytial virus
JOURNAL  Patent: WO 2004083373-A 44 30-SEP-2004;
THE UNIVERSITY OF NEWCASTLE UPON TYNE (GB)
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Score:          991.00      Matches:    191
Percent Similarity: 83.85%      Conservative: 27
Best Local Similarity: 73.46%      Mismatches: 40
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DB:             6           Gaps:      2

US-10-089-278-6 (1-329) x CQ881538 (1-897)

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Db      106  CCTGGGGTCTCAGCGAGGATTTCTGCAAGGATCCGGCTACACATTCTCATTTATGCT 165
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Qy      141  TyrTyrCysAlaArgSerAspGly---AsnTyrGlyTyrTyrTyrAlaLeuAspTyrTyr 159
Db      346  TATTACTGTGCAAGATCGGATATGATTACGGCCGGCGGGGTATGCTATGAGTACTGG 405
Qy      160  GlyGlnGlyThrThrValThrValSerSerGlyGlyGlyGlySerGlyGlyGlyGlySer 179
Db      406  GGCCAAGGGACCAACCGTCAACCGTCTCGAGTGTGGAGCGGTTTCAGGGCGAGGTGGCTCT 465
Qy      180  GlyGlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeu 199
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Qy      200  GlyGlnArgAlaThrIleSerCysArgAlaSerGluSer---ValAspSerTyrGlyAsp 218
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Db      586  ACCTATTTAGAGTGGTACCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAA 645
Qy      239  AlaSerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAsp 258
Db      646  GTTTCCAACCGATTTTCTGGGGTCCAGACAGAGTTTCAGTGGCAGTGGATCAGGGACAGAT 705
Qy      259  PheThrLeuThrIleAspProValGluGluAspAlaAlaValTyrTyrCysLeuGln 278
Db      706  TTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTACTGCTTTCAA 765
Qy      279  SerMetGluAspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAla 298
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Search completed: August 23, 2005, 15:48:23
Job time : 3953 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 23, 2005, 12:01:37 ; Search time 536 Seconds

(without alignments)
3633.573 Million cell updates/sec

Title: US-10-089-278-6

Perfect score: 1725

Sequence: 1 MDCLTLNLRAGKVDQASKI.....GSGGGGGGGGSGGASPVQFI 329

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Database :

N Geneseq 16Dec04:*

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SUMMARIES

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3	1202.5	69.7	946	5	Aaf61512 DNA encod
4	1186.5	68.8	927	5	Aaf61510 DNA encod
5	1094	63.4	868	10	ACC57513 Newcastle

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

6	1009.5	58.5	744	10	ADL07528
7	1004	58.2	906	5	Aaf61513
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11	992.5	57.5	969	4	Aaf30730
12	991	57.4	897	13	ADS88776
13	991	57.4	1698	3	AAZ43431
14	983	57.0	925	3	AAZ44206
15	983	57.0	925	3	AAZ58664
16	980	56.8	1010	4	Aaf73076
17	978	56.7	780	2	AAx06088
18	978	56.7	780	2	AAV81140
19	978	56.7	780	2	ADC63286
20	974.5	56.5	1817	8	ACC79607
21	948.5	55.0	1906	10	ADD13791
22	947.5	54.9	756	4	AA511887
23	946.5	54.9	891	2	AAT36907
24	935.5	54.2	717	4	AAC85539
25	935.5	54.2	717	10	AA151099
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30	924	53.6	2199	4	AAE30727
31	923.5	53.5	1734	4	AA889072
32	923	53.5	876	2	AAV10390
33	923	53.5	888	4	AAF30732
34	922.5	53.5	2214	13	ADR43336
35	920	53.3	1668	4	AA889071
36	920	53.3	1698	4	AA889073
37	920	53.3	1725	2	AAV01651
38	919	53.3	978	4	AAF30728
39	918.5	53.2	894	2	AAK33931
40	918	53.2	2952	6	ABK13464
41	917.5	53.2	1605	4	AAH78156
42	917.5	53.2	1605	6	ABA04532
43	917.5	53.2	1605	6	ABX00129
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ALIGNMENTS

RESULT 1
AAF61509
ID AAF61509 standard; DNA; 1030 BP.

XX AAF61509;

XX 11-SEP-2003 (revised)

DT 25-JUN-2001 (first entry)

XX DNA encoding SNV-env leader/human 7A5-scFv fusion construct.

XX T lymphocyte; antibody; single chain variable antibody; scFv; human;

KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;

KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;

KW acquired immune deficiency syndrome; severe combined immune deficiency;

KW T cell lymphoma; fusion construct; ds.

XX Homo sapiens.

OS Spleen necrosis virus.

OS Chimeric.

XX Key

XX Location/Qualifiers

FT CDS

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FT /product= "SNV-env leader peptide"

FT /note= "No stop codon given"

FT 179..1030

FT /tag= b

FT /product= "7A5-scFv"

FT /note= "no stop codon given"
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 XX 29-MAR-2001.
 XX
 XX 27-SEP-1999; 99DE-01046142.
 XX
 XX 27-SEP-1999; 99DE-01046142.
 XX
 PA (BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
 XX
 XX Cichutek K, Engelstaedter M;
 XX
 DR WPI; 2001-246140/26.
 DR P-PSDB; AAB70840.
 XX
 PT Cell-targeting vector selective for T lymphocytes, useful in gene therapy
 PT of e.g. acquired immune deficiency syndrome, encodes a single-chain
 PT variable antibody fragment.
 XX
 PS Claim 1; Fig 1; 18pp; German.
 XX
 XX This invention describes a novel cell-targeting vector (A) containing a
 CC DNA sequence (i) encoding a single-chain variable antibody fragment
 CC (scFv). The products of the invention have antiviral, cytostatic and
 CC immunostimulant activity and can be used in gene therapy, immunization
 CC and diagnosis particularly of T cell-associated diseases, specifically
 CC acquired immune deficiency syndrome (AIDS), severe combined immune
 CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
 CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
 CC human B cells, and 1000 fold selectivity over other human cells. A vector
 CC designated 7A5 encodes a 329 amino acid single-chain variable antibody
 CC fragment, fully defined in the specification. It was used to transform
 CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
 CC (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
 CC carcinoma) cells. After 48 hours, the cells were stained with X-gal to
 CC determine transformation. The viral titer (infectious units/ml) was over
 CC 1 million for D17, 1 million for C8166 but less than 100 for HeLa,
 CC showing the high selectivity for human T cells. This sequence encodes the
 CC SNV-env leader/human 7A5-scFv fusion construct used in the construction
 CC of novel cell targeting vectors described in the invention. (Updated on
 CC 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 1030 BP; 232 A; 244 C; 304 G; 250 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.57e-103 Length: 1030
 Score: 1725.00 Matches: 329
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0
 US-10-089-278-6 (1-329) x AAF61509 (1-1030)
 QY 1 MetAspCysLeuThrAsnLeuArgSerAlaGluGlyValAspGlnAlaSerLysile 20
 DB 44 ATGGACTGTCTCACCACCTCCAGTCCGTCGAGGGTAAGTTGACACAGGCGACAAATC 103
 QY 21 LeuIleLeuLeuValAlaTrpTrpGlyPheGlyThrThrAlaGluValSerThrAlaArg 40
 DB 104 CTAATTCCTCTTGGCTTGGTGGGGTTGGGACCACTCCCGAAGTTTCAGCTGCCCGA 163
 QY 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnGlnSerGlyAlaGluLeuValArg 60
 DB 164 GCGGCCCGCGCCATGGCCGAGGTCAAGCTGCAGCAGTCAGGGGCTGAGCTGGTGAGG 223
 QY 61 ProGlyValSerValLysIleSerCysLysGlySerGlyThrThrPheThrAspTyrGly 80
 DB 224 CCTGGGGTCTCAGTGAAGATTTCTCGACAGGGTCTGGCTACACATTCAGTGAATGCT 283

QY 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
 DB 284 ATGAGCTGGTCAAAACAGAGTCAATGCAAGAGTCTAGAGTGGATTGAGCTTATTAGTACT 343
 QY 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
 DB 344 TACTATGGTGTAGTCTTACCAACAGAGGTTCAAGGGCAAGGCCCAATGACTGTAGAC 403
 QY 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
 DB 404 AAATCTCTCCAACACAGAGCTTATTTGGAACTTGCAGACTGACATCTGAGGATTTGCCATT 463
 QY 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGly 160
 DB 464 TATTAATTGTGCAAGATCGGATGTAATTACGGGTATTACTATGCTTTGGACTACTGGGGC 523
 QY 161 GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 180
 DB 524 CAAGGCACCTACCGTCACTCCCTCAGGTGAGGCGGTTCAGGGCGAGGTGGCTCTGGC 583
 QY 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200
 DB 584 GGTGGCGGATCGGATATCGAGCTCACTCACTCTCCATCTCTTGGCTGTGTCTTAGGG 643
 QY 201 GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220
 DB 644 CAGAGGGCCACCATATCTCTGAGAGCCAGTGAAGTGTGTATAGTATTATGGCGATAGTTT 703
 QY 221 MetHisTrpTyrGlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArgAlaSer 240
 DB 704 ATGCACCTGTATTCAGCAGAAACAGGACAGCCACCAAACTCTCATCTATCTGTCATCC 763
 QY 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260
 DB 764 AACCTAGATCTGGAGTCCCTGCCAGTTCAGTGGCAGTGGTCTGAGTCAGACTTCACT 823
 QY 261 LeuThrIleAspProValGluGluAspAspAlaAlaValTyrTyrCysLeuGlnSerMet 280
 DB 824 CTCACCATCGATCTCTGGAGGAAGATGATGTCGAGTGTATTACTGTCTGCAAGATATG 883
 QY 281 GluAspProTyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAlaSer 300
 DB 884 GAAGATCCGTACACGTTCCGAGGGGGGCAAGCTGGAATAAAACGGGCGCGCATCG 943
 QY 301 GlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGly 320
 DB 944 GGCTCCGGGGGGGTGGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1003
 QY 321 SerGlyAlaSerProValGlnPheIle 329
 DB 1004 TCTGGCGCCAGGCCAGTCCAGTTTATC 1030
 RESULT 2
 AAF61511
 ID AAF61511 standard; DNA; 990 BP.
 XX
 XX AAF61511;
 XX
 XX 11-SEP-2003 (revised)
 DT 25-JUN-2001 (first entry)
 XX
 XX DNA encoding SNV-env leader/human 7B2-scFv fusion construct.
 XX
 XX T lymphocyte; antibody; single chain variable antibody; scFv; human;
 KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
 KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
 KW acquired immune deficiency syndrome; severe combined immune deficiency;
 KW T cell lymphoma; fusion construct; ds.
 XX
 OS Homo sapiens.
 OS Spleen necrosis virus.
 OS Chimeric.
 XX

PH	Key	Location/Qualifiers	QY	41	AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg	60
FT	CDS	1..135	DB	121	GCAGCCAGCCGCCCATGGCCAGGTGCAGTGCAGCAGTCTGGAGTGAACCAACA	180
FT		/*tag= a				
FT		/product= "SNV-env leader peptide"				
FT		/note= "No stop codon given"				
FT	CDS	136..990	QY	61	ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly	80
FT		/*tag= b	DB	181	CTTGGGGCCTCAGTGGAGATGCTCTGCNAGGCTTCTGGCTACGCCCTTACTACTCTGG	240
FT		/product= "7B2-scFv"				
FT		/note= "no stop codon given"				
FT		/partial				
XX	DE19946142-A1.		QY	81	MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIle	98
XX			DB	241	ATGCACTGGGTAACACAGAGCCCTGGACAGGGTCTGGATGGATTGGATACATTAACTCT	300
XX	29-MAR-2001.		QY	99	SerThrTyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThr	118
XX			DB	301	ACCACTGATTATTAATCTGAC-----TACAATCTCAAGTTCAAGGACCAAGGCCACATTGACT	354
XX	27-SEP-1999; 99DB-01046142.		QY	119	ValAspLysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSer	138
XX			DB	355	GCAGACAAATCCTCCAGTACAGCTACATGCACTGAGCAGCCTGACATCTGAGGACTCT	414
XX	27-SEP-1999; 99DE-01046142.		QY	139	AlaIleTyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyr	158
XX	(BUND) BUNDESREPUBLIK DEUT PAUL-EHRlich-INST.		DB	415	GCAGTCTATTACTGTGCAAGATCG-----GGTGGTCTCTATGCTATGCACTAC	462
XX	Cichutek K, Engelstaedter M;		QY	159	TrpGlyGlnGlyThrThrValSerSerGlyGlyGlyGlyGlySerGlyGlyGly	178
XX	WPI; 2001-246140/26.		DB	463	TGGGGGCAAGGGACCAACCGTCACTCTCTCAGGTGGAGCGGTTCAGCGGAGGTGGC	522
XX	P-PSDB; AAB70842.		QY	179	SerGlyGlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSer	198
XX	Cell-targeting vector selective for T lymphocytes, useful in gene therapy		DB	523	TCGGGGTGGGGATCGGACATCGAGCTCAGTCTCCAGCAATCATGTCTGCACTCT	582
XX	of e.g. acquired immune deficiency syndrome, encodes a single-chain		QY	199	LeuGlyGlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAsp	218
XX	variable antibody fragment.		DB	583	CCAGGGGAGAAGGTCAACCACTGCAGTGCAGCTCAAGTGTGTA-----	627
XX	Claim 1; Fig 3; 18pp; German.		QY	219	SerPheMetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArg	238
XX	This invention describes a novel cell-targeting vector (A) containing a		DB	628	AGTTACATGCACCTGGTTCCAGCAGAGCCAGGCAGCTTCTCCCAAACTCTGGATTATAGC	687
XX	DNA sequence (I) encoding a single-chain variable antibody fragment		QY	239	AlaSerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAsp	258
XX	(scFv). The products of the invention have antiviral, cytostatic and		DB	688	ACATCCAACTGGCTCTGGAGTCTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGT	747
XX	immunostimulant activity and can be used in gene therapy, immunization		QY	259	PheThrLeuThrIleAspProValGluGluAspAspAlaAlaValTyrTyrCysLeuGln	278
XX	and diagnosis particularly of T cell-associated diseases, specifically		DB	748	TACTCTCTCAATCAGCCGAATGGAGGTGGAAGATGCTGCCACTTATTACTGCCAGCA	807
XX	acquired immune deficiency syndrome (AIDS), severe combined immune		QY	279	SerMetGluAspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAla	298
XX	deficiency (SCID) or T cell lymphoma. (A) target T cells, independently		DB	808	AGGAGTAGTATCCCATTCAGTTCGGCTCGGGCACCAGCTGGAAATCAAAACGGCGGCC	867
XX	of the CD4 receptor, with high selectivity. 4-5 fold selectivity over		QY	299	AlaSerGlySerGlyGlyGlySer---GlyGlyGlySerGlyGlyGlyGlySerGly	317
XX	human B cells, and 100 fold selectivity over other human cells. A vector		DB	868	GCATCGGGTCTCGGGGGCGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGT	927
XX	designated 7A5 encodes a 329 amino acid single-chain variable antibody		QY	318	GlyGlyGlySerGlyAlaSerProValGlnPheIle	329
XX	fragment, fully defined in the specification. It was used to transform		DB	928	GGTGGTGGTCTTCTGGCGCCAGCCAGTCCAGTCCAGTTCATC	963
XX	D17 (canine osteosarcoma cells susceptible to spleen necrosis virus					
XX	(SNV) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical					
XX	carcinoma) cells. After 48 hours, the cells were stained with X-gal to					
XX	determine transformation. The viral titer (infectious units/ml) was over					
XX	1 million for D17, 1 million for C8166 but less than 100 for HeLa,					
XX	showing the high selectivity for human T cells. This sequence encodes the					
XX	SNV-env leader/human 7B2-scFv fusion construct used in the construction					
XX	of novel cell targeting vectors described in the invention. (Updated on					
XX	11-SEP-2003 to standardise OS field)					
XX	Alignment Scores:					
XX	Pred. No.:	5.84e-72	Length:	990		
XX	Score:	1239.00	Matches:	243		
XX	Percent Similarity:	82.23%	Conservative:	30		
XX	Best Local Similarity:	73.19%	Mismatches:	45		
XX	Query Match:	71.83%	Indels:	14		
XX	DB:	5	Gaps:	5		
XX	Sequence 990 BP; 210 A; 263 C; 289 G; 228 T; 0 U; 0 Other;					
XX	US-10-089-278-6 (1-329) x AAF61511 (1-990)					
QY	1	MetAspCysLeuThrAsnLeuArgSerAlaGluGlyLysValAspGlnAlaSerLysIle	20			
DB	1	ATGGAGTGTCTACCAACCTCCGATCGCTGAGGGTAAAGTTGACCGAGCGGACCAAAATC	60			
QY	21	LeuIleLeuLeuValAlaTrpTrpGlyPheGlyThrThrAlaGluValSerThrAlaArg	40			
DB	61	CTAAATCTCTGCTGGTGGTGGGTTGGGACCACTGCCGAAGTTTCGACTGCGCGCA	120			
DE	DNA encoding SNV-env leader/human 7E4-scFv fusion construct.					
XX	T lymphocyte; antibody; single chain variable antibody; scFv; human;					
KW	cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;					

KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
 KW acquired immune deficiency syndrome; severe combined immune deficiency;
 KW T cell lymphoma; fusion construct; ds.

XX Homo sapiens.
 OS Spleen necrosis virus.
 OS Chimeric.

Key Location/Qualifiers
 CDS 1..135
 FT /tag= a
 FT /product= "SNV-env leader peptide"
 FT /note= "No stop codon given"
 FT 136..946
 CDS
 FT /tag= b
 FT /product= "7E4-scfv"
 FT /note= "no stop codon given"
 FT /partial

XX DE19946142-A1.

XX 29-MAR-2001.

XX 27-SEP-1999; 99DE-01046142.

XX 27-SEP-1999; 99DE-01046142.

XX (BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.

XX Cichutek K, Engelstaedter M;

XX WPI; 2001-246140/26.

DR P-PSDB; AAB70843.

XX Cell-targeting vector selective for T lymphocytes, useful in gene therapy
 of e.g. acquired immune deficiency syndrome, encodes a single-chain
 variable antibody fragment.

XX Claim 1; Fig 4; 18pp; German.

XX This invention describes a novel cell-targeting vector (A) containing a
 DNA sequence (1) encoding a single-chain variable antibody fragment
 (scFv). The products of the invention have antiviral, cytostatic and
 immunostimulant activity and can be used in gene therapy, immunization
 and diagnosis particularly of T cell-associated diseases, specifically
 acquired immune deficiency syndrome (AIDS), severe combined immune
 deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
 of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
 human B cells, and 1000 fold selectivity over other human cells. A vector
 designated 7A5 encodes a 329 amino acid single-chain variable antibody
 fragment, fully defined in the specification. It was used to transform
 CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
 (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
 carcinoma) cells. After 48 hours, the cells were stained with X-gal to
 determine transfection. The viral titer (infectious units/ml) was over
 CC 1 million for D17, 1 million for C8166 but less than 100 for HeLa.
 CC The high selectivity for human T cells. This sequence encodes the
 CC SNV-env leader/human 7E4-scfv fusion construct used in the construction
 of novel cell targeting vectors described in the invention. (Updated on
 CC 11-SEP-2003 to standardise OS field)

SQ Sequence 946 BP; 199 A; 249 C; 276 G; 222 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.32e-69 Length: 946
 Score: 1202.50 Matches: 236
 Percent Similarity: 83.12% Conservative: 30
 Best Local Similarity: 73.75% Mismatches: 47
 Query Match: 69.71% Indels: 7
 DB: 5 Gaps: 4

US-10-089-278-6 (1-329) x AAF61512 (1-946)

QY	1	MetAspCysLeuThrAsnLeuArgSerAlaGluGlyLysValAspGlnAlaSerLysIle	20
DB	1	ATGGACTGCTCACCACCTCCGATCCGCTGAGGGTAAAGTTGACACGCGAGCAAAATC	60
QY	21	LeuIleLeuValAlaIleTTPGlyPheGlyThrThrAlaGluValSerThrAlaArg	40
DB	61	CTAATTCCTCTTGGCTTGGTGGGGGTTGGGACCACTGCCGAAAGTTTCGACTGCCGA	120
QY	41	AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyValaGluLeuValArg	60
DB	121	GGGGCCACGCGCCATGGCCGAGGTCAAGCTGCAGCAGTCAGGGCTCAGCTGGTGGG	180
QY	61	ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly	80
DB	181	CTGGAGCTTCAGTGAAGCTGCTCTGCAAGACTTCTGGCTTCTCTTCCACAGCTACTG	240
QY	81	MetSerTTPValLysGlnSerHisAlaLysSerLeuGluTTPIleGlyLeuLeuSerThr	100
DB	241	ATGAACCTGGCTGAAGCTGAGGCTCGACAAAGCCCTTGAAGTGGATGGCATGATTCCT	300
QY	101	TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp	120
DB	301	TCCGATAGTGAACCTAGTTTAACTCAGAGGTTCAAGGACAGCCACACTGACTGTAGAC	360
QY	121	LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle	140
DB	361	AAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCGACATCTCAGGACTCTCGCGTC	420
QY	141	TyrTyrCysAlaArgSer---AspGlyAsnTyrGlyTyrTyrThrAlaLeuAspTyrTTP	159
DB	421	TATTACTGTCAAGATCTCTTTATGCTAACTACCCCTCCTCGTTTACT-----TACTGG	474
QY	160	GlyGlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlyGlySer	179
DB	475	GGCCAGGACACACCGCTCACCCTCCTCAGGTGGAGCGGTTTCAGCCGAGGTGGCTCT	534
QY	180	GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeu	199
DB	535	GGCGTGGCGGATCGGACATCGAGCTCACTCAGTCTCCACACCACCTGCTGCTCCTCC	594
QY	200	GlyGlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSer	219
DB	595	GGGGAGAGATCACTATCACTGCGAGTCCAGTCAAGTATAGTTTCC-----AAT	645
QY	220	PheMetHisTTPTrpGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArgAla	239
DB	646	TACTTCATTTGGTATCAGCAGAGACCGAGATTCCTCCCTAACTCTTGATTATAGACA	705
QY	240	SerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPhe	259
DB	706	TCCAACTCGCTTCGGAGTCCCGAGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTAC	765
QY	260	ThrLeuThrIleAspProValGluGluAspAlaAlaValTyrTyrCysLeuGlnSer	279
DB	766	TCTCTCACAATTTGGCACCACTGGAGGTGAAGATGTTGCCACTTACTTCTGCCAGCGGT	825
QY	280	MetGluAspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAla	299
DB	826	AGTAGTATACCGTACACGTTGGAGGGGGGACCAAGCTGGAAATAAAGCGGCGGCCGA	885
QY	300	SerGlySerGlyGlyGlySer---GlyGlyGlySerGlyGlyGlySerGlyGly	318
DB	886	TCGGGCTCCGGGGCGGTGTTCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	945
XX	RESULT 4		
XX	AAF61510		
XX	ID	AAF61510	standard; DNA; 927 BP.
XX	AC	AAF61510;	
XX	DT	11-SEP-2003	(revised)
XX	DT	25-JUN-2001	(first entry)

DE DNA encoding SNV-env leader/human K6-scfv fusion construct.

XX T lymphocyte; antibody; single chain variable antibody; scFv; human;
 KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
 KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
 KW acquired immune deficiency syndrome; severe combined immune deficiency;
 KW T cell lymphoma; fusion construct; ds.

XX Homo sapiens.

OS Spleen necrosis virus.

OS Chimeric.

XX Key Location/Qualifiers

CDS 1..135

FT /*tag= a

FT /product= "SNV-env leader peptide"

FT /note= "No stop codon given"

CDS 136..927

FT /*tag= b

FT /product= "K6-scfv"

FT /note= "no stop codon given"

FT /partial

XX DE19946142-Al.

XX 29-MAR-2001.

XX 27-SEP-1999; 99DE-01046142.

XX 27-SEP-1999; 99DE-01046142.

XX (BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.

XX Cichutek K, Engelstaedter M;

XX WPI; 2001-246140/26.

XX P-PSDB; AAB70841.

XX Cell-targeting vector selective for T lymphocytes, useful in gene therapy
 of e.g. acquired immune deficiency syndrome, encodes a single-chain
 variable antibody fragment.

XX Claim 1; Fig 2; 18pp; German.

XX This invention describes a novel cell-targeting vector (A) containing a
 DNA sequence (I) encoding a single-chain variable antibody fragment
 (scFv). The products of the invention have antiviral, cytostatic and
 immunostimulant activity and can be used in gene therapy, immunization
 and diagnosis particularly of T cell-associated diseases, specifically
 acquired immune deficiency syndrome (AIDS), severe combined immune
 deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
 of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
 human B cells, and 1000 fold selectivity over other human cells. A vector
 designated 7A5 encodes a 329 amino acid single-chain variable antibody
 fragment, fully defined in the specification. It was used to transform
 D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
 (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
 carcinoma) cells. After 48 hours, the cells were stained with X-gal to
 determine transformation. The viral titer (infectious units/ml) was over
 1 million for D17, 1 million for C8166 but less than 100 for HeLa.
 CC showing the high selectivity for human T cells. This sequence encodes the
 SNV-env leader/human K6-scfv fusion construct used in the construction of
 CC novel cell targeting vectors described in the invention. (Updated on 11-
 CC SEP-2003 to standardise OS field)

XX Sequence 927 BP; 205 A; 238 C; 277 G; 207 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.:	1.41e-68	Length:	927
Score:	1186.50	Matches:	229
Percent Similarity:	79.69%	Conservative:	26
Best Local Similarity:	71.56%	Mismatches:	54
Query Match:	68.78%	Indels:	11

DB:	5	Gaps:	2
US-10-089-278-6 (1-329) x AAF61510 (1-927)			
Qy	1 MetAspCysLeuThrAsnLeuArgSerAlaGluGlyValAspGlnAlaSerLysLeu	20	
Db	1 ATGGACTGTCTCACCAACCTCCGATCCGCTGAGGTAAGTTGACCAGCGGAGCAAAATC	60	
Qy	21 LeuLeuLeuValAlaThrTrpGlyPheGlyThrThrAlaGluValSerThrAlaArg	40	
Db	61 CTAATTCTCTCTGTGGCTTGTGGGGTTTGGGACCACTGCCGAAGTTTGGACTGCCGA	120	
Qy	41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg	60	
Db	121 GCGGCCAGCCGGCCATGGCCGAGGTCACCTCAGAGGTCAGGACTGAGACTGAACCTGTGAAG	180	
Qy	61 ProGlyValSerValLysLysSerCysLysGlySerGlyThrThrPheThrAspTyrGly	80	
Db	181 CCTGGGGCTTCAGTGAATCTGTCTTGCAGGCTTCTGGCTACACCTTCCACGACTACTGG	240	
Qy	81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpLysLeuLeuSerThr	100	
Db	241 ATGCACCTGGTTGAAGCAGAGGCTTGGACAGGCTTGGTGGATCGGAGAGATTGATCCT	300	
Qy	101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp	120	
Db	301 GTTGATAGTTATTAATACTAACAATAAATCAAGGGCAAGGCCACACTGACTGTAGAC	360	
Qy	121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle	140	
Db	361 AAGTCTCCACCACAGCTACATGACCTCAGCAGGCTGACATCTGAGGACTCTCGCGTC	420	
Qy	141 TyrTyrCysAlaArgSerAspGlyAsnTyrTyrTyrTyrAlaLeuAspTyrTrpGly	160	
Db	421 TATTACTGTGCAAGAAAGGCGC-----TATGCTATGACTACTGCGGC	462	
Qy	161 GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlyGlySerGly	180	
Db	463 CAAGGACCAACGTCACCTCCTCAGGTGGATGCGGTTCCAGCGGAGGTGGCTCTCGGC	522	
Qy	181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly	200	
Db	523 GGTGGCGGATCGGACATCGAGCTCACTCAGTCACCAAGCAATCATGTCTGCATCTCCAGG	582	
Qy	201 GlnArgAlaThrLysSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe	220	
Db	583 GAGAGGTCACCATGACCTGCGAGTGCAGTGCAGCTCAAGTATA-----AGTTAC	627	
Qy	221 MetHisTrpTrpGlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArgAlaSer	240	
Db	628 ATGCATGGTACCAGCAGAGGAGCCAGGACCTCCCCCAAGATGGGATTTATGACACATCC	687	
Qy	241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr	260	
Db	688 AAATGGCTTCGGAGTCCCTGCTGCTCAGTGGCAGTGGGCTCGGACCTCTTATTCT	747	
Qy	261 LeuThrIleAspProValGluGluAspAlaValTyrTyrCysLeuGlnSerMet	280	
Db	748 CTCCCAATCAGCAGCATGGAGGCTGAAGATGCTGCCACTTATTACTGCCATCAGCGAGT	807	
Qy	281 GluAspProTyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAlaSer	300	
Db	808 AGTTACCCATGGACGTTCCGTTGGAGGAGCAACAGCTGAAATAAAGCGGCGGCGCATCG	867	
Qy	301 GlySerGlyGlyGlySerGlyGlySerGlyGlyGlyGlyGlyGlyGlyGlyGlyGly	320	
Db	868 GGGTCCGGGGGGGGTGGTCTGGTGGTGGTCTGGTGGTGGTCTGGTGGTGGTGGT	927	
RESULT 5			
ACC57513			
ID	ACC57513	standard; cDNA; 868 BP.	
XX			
AC	ACC57513;		

XX This invention describes a novel cell-targeting vector (A) containing a
 CC DNA sequence (1) encoding a single-chain variable antibody fragment
 CC (scFv). The products of the invention have antiviral, cytostatic and
 CC immunostimulant activity and can be used in gene therapy, immunization
 CC and diagnosis particularly of T cell-associated diseases, specifically
 CC acquired immune deficiency syndrome (AIDS), severe combined immune
 CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
 CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
 CC human B cells, and 1000 fold selectivity over other human cells. A vector
 CC designated 7A5 encodes a 329 amino acid single-chain variable antibody
 CC fragment, fully defined in the specification. It was used to transform
 CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
 CC (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
 CC carcinoma) cells. After 48 hours, the cells were stained with X-gal to
 CC determine transformation. The viral titer (infectious units/ml) was over
 CC 1 million for D17, 1 million for C8166 but less than 100 for HeLa,
 CC showing the high selectivity for human T cells. This sequence encodes the
 CC SNV-env leader/human 6C3-scFv fusion construct used in the construction
 CC of novel cell targeting vectors described in the invention. (Updated on
 CC 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 906 BP; 204 A; 246 C; 262 G; 194 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,01e-56 Length: 906
 Score: 1004.00 Matches: 196
 Percent Similarity: 78.90% Conservative: 47
 Best Local Similarity: 63.64% Mismatches: 51
 Query Match: 58.20% Indels: 14
 DB: 5 Gaps: 4

US-10-089-278-6 (1-329) x AAF61513 (1-906)

Qy 1 MetAspCysLeuThrAenLeuArgSerAlaGluLysValAspGlnAlaSerLysLeu 20
 Db 1 ATGGACTGTCTCCACCACTCCGATCCGCTGAGGGTAAAGTTGACAGGGGAGCAAAATC 60
 Qy 21 LeuileuLeuValAlaTTPGlyPheGlyThrThrAlaGluValSerThrAlaArg 40
 Db 61 CTAAATCTCTTGGGCTTGGTGGGGTGTGGGACCACTCCCGAAGTTTCGATGCCCCGA 120
 Qy 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg 60
 Db 121 CGGGCCAGCGGCCATGGCCAGTACAGCTGACAGCTGACGAGCAGAGAAATGAAAAG 180
 Qy 61 ProGlyValSerValLysLeuSerCysLysGlySerGlyThrThrPheThrAspTyrGly 80
 Db 181 CCGGGGAGTCTCTGAAAATCTCTGTAAAGGGTTTGGATACGACTTTAGCACTACTGG 240
 Qy 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuLeuSerThr 100
 Db 241 ATCGCTGGTGGCCAGATGCCGGGAAAGGCTGGAGTACATGGGGCTCATCTATCCT 300
 Qy 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
 Db 301 GGTGACTCTGACCAATATACAGCCCTCTTCAAGGCCAGGTCACCATCTCAGCCGAC 360
 Qy 121 LysSerSerAenThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
 Db 361 AAGTCCATCAGCAGCGCTACCTGACGTGGAGCAGCCTGAAGGCTCGGACACCGCCATG 420
 Qy 141 TyrTyrCysAlaArgSerAspGly-----AenTyrGlyTyr 152
 Db 421 TATTACTGTGCGAGAGTCTCTGGATATTGTAGTAGTACCAAGCTGCTATGACTAC---TAC 477
 Qy 153 TyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrThrValThrValSerSerGlyGly 172
 Db 478 TACTACTACATGAGCTGTGGGCGCGGGAACTGTGTCACCTCTCAGAGGTGGAGGC 537
 Qy 173 GlySerGlyGlyGlySerGlyGlyGlySerAspIleGluLeuThrGlnSerPro 192
 Db 538 GGTTCAGGCGAGGTGCTCTGGCGGTGGGGATCGGACATCGTGATGACCCGCTCCT 597

Qy 193 SerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCysArgAlaSerGluSer 212
 Db 598 TCACCTCTGTCATCTGTAGAGACAGAGTCACCATGACTTGCAGGCGCCAGTCAGAAC 657
 Qy 213 ValAspSerTyrGlyAspSerPheMetHisTyrTyrGlnGlnLysProGlyGlnProPro 232
 Db 658 ATTAATATCTGG-----TTGGCTCGTATCAGCAGAAACACAGGAAAGCCCT 705
 Qy 233 LysLeuLeuIleTyrArgAlaSerAenLeuGluSerGlyValProAlaArgPheSerGly 252
 Db 706 AAGTCTCTGATCTATAAGCGCTCCACTTTAGAGAGTGGGCTCCCGTCAAGGTTTCAGCGC 765
 Qy 253 SerGlySerGluSerAspPheThrLeuThrIleAspProValGluGluAspAlaAla 272
 Db 766 AGTGGATCTGGGACAGAAATCTCTCACATCAGCGGCTGCGAGCTGATGATTTTGA 825
 Qy 273 ValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGlyGlyThrLysLeu 292
 Db 826 AGTTATTACTGT--CAACGGTATGATAGTACTGCTGCTGGCCCAAGGACCAAGCTG 882
 Qy 293 GluIleLysArgAlaAlaAlaSer 300
 Db 883 GAGATCAATACGTGGCGCCGATCG 906
 RESULT 8
 ID AAA60982 standard; DNA; 1094 BP.
 AC AAA60982;
 DT 08-NOV-2000 (first entry)
 XX Antibody nucleotide sequence.
 DE Lida-protein; LDP; Lida-chromophore; LDC; antibody; lidamycin;
 KW antibiotic; anticancer; tumour; cancer; ds.
 OS Synthetic.
 XX CN1251840-A.
 XX 03-MAY-2000.
 XX 13-OCT-1999; 99CN-00121668.
 XX 13-OCT-1999; 99CN-00121668.
 XX (MEDI-) INST MEDICINAL BIOTECHNOLOGY CHINESE ACA.
 XX Zhen Y, Li S, Jiang M;
 XX WPI; 2000-432052/38.
 XX Constitutive fusion protein of ridamycin as anticancer antibiotic and
 XX single-chain antibody.
 XX Disclosure; Page 2-3; 18pp; Chinese.
 The present invention describes a fusion protein, designated Lidamycin,
 composed of Lida-protein (LDP) and Lida-chromophore (LDC), which acts as
 an anticancer antibiotic and single-chain antibody. LDP and LDC are
 joined via non-covalent bonds and can be splitted and recombined. A
 single-chain antibody scFv can specifically join with IV-type collagenase
 and can suppress its activity and in order to increase the permeability
 of medicine to capillary tubes and the penetrability to real tumour, DNA
 recombination and molecular recombination are used to prepare new-type
 constitutive fusion protein LDM-Fv of anticancer targeting medicine
 CC Lidamycin and single-chain antibody. Its molecular weight is about 37kDa.
 CC It has the activity to inhibit IV-type collagenase and strong intrusion-
 CC resistance kill action to cancer cells. It may be an ideal clinic
 CC medicine. The present sequence represents an antibody nucleotide sequence
 CC given in the exemplification of the present invention

Score:	993.50	Matches:	195
Percent Similarity:	83.85%	Conservative:	23
Best Local Similarity:	75.00%	Mismatches:	39
Query Match:	57.59%	Indels:	3
DB:	4	Gaps:	2
US-10-089-278-6 (1-329) x AAF30729 (1-2190)			
QY	41	AlaAlaGlnProAlaMetAlaGluValLysLeuGlnGlnSerGlyAlaGluLeuValArg	60
DB	46	GCAGCCAGCCGCGCCAGTGGCCGAGGTTTCAGCTTCAGCAGTCTGGACTGAGCTGGTGAAG	105
QY	61	ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly	80
DB	106	CCCGGGCCCTCAGTGAAGATTTCTGCAAGCTTCTGGCTACGCATTCAGTAGCTCTTGG	165
QY	81	MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr	100
DB	166	ATGAACCTGGGTGAAGCAGAGCCCTGGACAGGGTCTTCAGTGGATTGGACGGATTATCCT	225
QY	101	TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp	120
DB	226	GGAAATGGAGATCACTACATCAATGGAGGTTCAAGGCAAGGCCACACTGACTGCAGAC	285
QY	121	LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle	140
DB	286	ANATCTCCAGCAGACCTACATCAGCTCAGCAGCCTGACCTCTGTGGACTCTGCGGTC	345
QY	141	TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGly	160
DB	346	TATTTCTGTGCA-----GATGTAACGTA---TATTACTATCTATGGACTACTGGGT	396
QY	161	GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly	180
DB	397	CAGGAACCTCAGTACCGTCTCTCAGGTGGAGCGGTTTCAGTGGCGCGCTCTGGC	456
QY	181	GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly	200
DB	457	GGTGGCGGATCGCAATTTGTTCTCACCCAGTCTCTCTCTCTCTCTCTCTCTCTCTCT	516
QY	201	GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe	220
DB	517	CAGAGGCCACCATCTCATGCGAGGCCAGCAAAAGTGTCACTACATCTGGCTATAGTTAT	576
QY	221	MetHisTrpTyrGlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArgAlaSer	240
DB	577	ATGCATCTGGTACCACAGAAACAGACAGCCACCCAACTCTCTATCTATCTTGTATCC	636
QY	241	AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr	260
DB	637	AACCTAGAATCTGGGTCTCTGCGAGGTTTCAGTGGCAGTGGTCTGGACAGACTTCACC	696
QY	261	LeuThrIleAspProValGluGluAspAlaValTyrTyrCysLeuGlnSerMet	280
DB	697	CTCAACATCCATCTGTGGAGGAGGAGTGTGCAACCTATTACTGTCTCAGACAGTAGG	756
QY	281	GluAspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAlaSer	300
DB	757	GAGTCTCTCGGAGTTCGGTGGAGGCCACCAAGCTGGAAATCAACGGCGCGCGAGCC	816
RESULT 10			
AAF30734			
ID	AAF30734 standard; DNA; 876 Bp.		
XX			
AC	AAF30734;		
XX			
DT	21-JUN-2001 (first entry)		
XX			
DE	DNA encoding antibody 8860 scFv with c-myc-tag.		
XX			
KW	Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;		
KW	Factor VIII cofactor; blood coagulation disorder; haemophilia A;		
KW	haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse; myc-tag;		

KW	ds.
XX	Mus musculus.
OS	Synthetic.
OS	Escherichia coli.
OS	Chimeric.
XX	Key
FT	CDS
FT	1..876
FT	/*tag= a
FT	sig_peptide
FT	1..86
FT	/*tag= b
FT	mat_peptide
FT	67..873
FT	/*tag= c
XX	WO200119992-A2.
PN	22-MAR-2001.
XX	13-SEP-2000; 2000WO-EP008936.
XX	14-SEP-1999; 99AT-00001576.
PR	(BAXT) BAXTER AG.
XX	Scheiflinger F, Kerschbaumer R, Falkner F, Dörner F;
PI	WPI; 2001-290358/30.
XX	P-PSDB; AAB20443.
DR	New factor IX/factor IXa antibodies and their derivatives useful for
XX	increasing amidolytic activity of factor IXa, and for treating blood
PT	coagulation disorders such as hemophilia A and hemorrhagic diathesis.
PT	Example 18; Fig 35; 138pp; English.
XX	The present sequence is that of DNA encoding a fusion protein (see
CC	AAB20443) comprising (from the N-terminal end): a PelB leader sequence; a
CC	single chain Fv (scFv) derivative of antibody 8860 comprising the heavy
CC	(VH) and light (VL) chain variable regions of 8860 joined by an
CC	artificial flexible linker peptide; a Myc-tag and a C-terminal 6His
CC	affinity tail. The fusion protein was expressed in Escherichia coli from
CC	vector pMYH16. The construct was used as a negative control to
CC	determine the Factor VIII (FVIII)-like activity of a 198/B1 antibody scFv
CC	fragment (see AAB20442) also expressed from pMYH16. 198/B1 (clone AB2)
CC	is an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)
CC	antibodies of the invention. Anti-FIX/FIXa antibodies and their
CC	derivatives, including scFv fragments, have FVIII cofactor activity or
CC	FIXa activating activity. Administration leads to an increase in the
CC	procoagulant activity of FIXa, even in the presence of FVIII inhibitors.
CC	This allows for rapid blood coagulation even in the absence of FVIII or
CC	FVIIIa, and in the case of FVIII inhibitor patients. The antibodies and
CC	derivatives are used in a claimed pharmaceutical composition for treating
CC	patients with blood coagulation disorders, especially haemophilia A and
CC	haemorrhagic diathesis
XX	Sequence 876 Bp; 211 A; 233 C; 239 G; 193 T; 0 U; 0 Other;
SQ	Alignment Scores:
	Pred. No.: 5,44e-56 Length: 876
	Score: 992.50 Matches: 195
	Percent Similarity: 83.78% Conservative: 22
	Best Local Similarity: 75.29% Mismatches: 39
	Query Match: 57.54% Indels: 3
	DB: 4 Gaps: 2
US-10-089-278-6 (1-329) x AAF30734 (1-876)	
QY	41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnGlnSerGlyAlaGluLeuValArg 60
DB	46 GCAGCCAGCCGCGCCAGTGGCCGAGGTTTCAGCTTCAGCAGTCTGGACTGAGCTGGTGAAG 105
QY	61 ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80

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Db 106 CCGGGGCTCAGTGAAGATTCTCGAAGCTTCCTGCTAGCAATTCAGTACTCTTGG 165
Qy 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
Db 166 ATGAACCTGGGTGAAGCAGAGCCCTGGACAGGGTCTTGAGTGGATTGGACGGATTATCCT 225
Qy 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db 226 GGAATGGAGATACATAATGGAAGTTCAAGGGCAAGGCCACACTGACTGCAGAC 285
Qy 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db 286 AATCTCTCCAGCAGACCTACATCAGCTCAGCAGCCTGACCTCTGAGACTCTGCGGTC 345
Qy 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGly 160
Db 346 TATTTCTGTGCA-----GATGGTAACGTA---TATTACTATGCTATGGACTACTGGGT 396
Qy 161 GlnGlyThrThrValThrValSerGlyGlyGlyGlySerGlyGlyGlyGlySerGly 180
Db 397 CAAGAACTTCAGTCCCGTCTCTCAGGTGGAGCGGTTCAAGTGGCGCGCTCTGGC 456
Qy 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200
Db 457 GGTGGCGGATCGCAATGTTCTCACCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGGG 516
Qy 201 GlnArgAlaThrIleSerCysArgAlaSerGlnSerValAspSerTyrGlyAspSerPhe 220
Db 517 CAGAGGCCACCATCTCATCAGGCCAGCAAAAGTGTGCTAGTATCATCTGGCTATAGTTAT 576
Qy 221 MetHisTrpTyrGlnGlnLysProGlyGlnProProLysLeuLeuLeuTyrArgAlaSer 240
Db 577 ATGCAGCTGGTACCAACAGAACAGGACAGCCAACTCTCATCTATCTTGTGATCC 636
Qy 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260
Db 637 AACTAGATCTGGGTCTCTGCCAGTTTCAGTGGCAGTGGTCTGGACAGACTTCACC 696
Qy 261 LeuThrIleAspProValGluGluAspAlaValTyrTyrCysLeuGlnSerMet 280
Db 697 CTCAACATCCATCTCTGGAGGAGGAGGAGTCTGCAACCTATTACTGTGCAGCAGTAGG 756
Qy 281 GluAspProTyrThrPheGlyGlyGlyThrLysLeuGluLeuLysArgAlaAla 299
Db 757 GAGCTTCTCCGACGTTCGGTGGAGCACCAGCTGGAATCAACGGCGCGCGCA 813

RESULT 11
AAF30730
ID AAF30730 standard; DNA; 969 BP.
XX
AC AAF30730;
XX
DT 21-JUN-2001 (first entry)
XX
DE Antibody 8860 bivalent miniantibody DNA.
XX
KW Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant;
KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
KW bivalent antibody; p8860-Zip1.2; ds.
XX
OS Mus musculus.
OS Synthetic.
OS Escherichia coli.
OS Chimeric.
XX
PH Key Location/Qualifiers
CDS 1..969
FT /*tag= a
FT sig_peptide 1..66
FT /*tag= b
FT /*note= "PelB leader sequence"
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FT mat_peptide 67..966
PT /*tag= c
XX
PN WO200119992-A2.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-EP008936.
XX
PR 14-SEP-1999; 99AT-00001576.
XX
PA (BAXT ) BAXTER AG.
XX
PI Scheifflinger F, Kerschbaumer R, Falkner F, Dörner F;
XX
DR WPI; 2001-290358/30.
DR P-PSDB; AAB20440.
XX
PT New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX
PS Example 16; Fig 30; 138pp; English.
XX
CC The present sequence is that of the coding region of plasmid p8860-
CC Zip#1.2 encoding a bivalent miniantibody (see AAB20440) comprising the
CC single chain Fv (scFv) fragment of antibody 8860 fused to an amphipathic
CC helical structure. The plasmid was obtained by inserting 8860 scFv DNA
CC into vector pZipl. The construct was used as negative control in
CC examination of the Factor VIII (FVIII)-like activity of an antibody
CC 193/B1 miniantibody (see AAB20438). 193/B1 is an example of anti-human
CC Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the invention.
CC Anti-FIX/FIXa antibodies and their derivatives have FVIII cofactor
CC activity or FIXa activating activity. Administration leads to an increase
CC in the procoagulant activity of FIXa, even in the presence of FVIIIa
CC inhibitors. This allows for rapid blood coagulation even in the absence
CC of FVIII or FVIIIa, and in the case of FVIII inhibitor patients. The
CC antibodies and derivatives are used in a claimed pharmaceutical
CC composition for treating patients with blood coagulation disorders,
CC especially haemophilia A and hemorrhagic diathesis. The present bivalent
CC miniantibody exhibited no FVIII-like activity
XX
SQ Sequence 969 BP; 233 A; 257 C; 264 G; 215 T; 0 U; 0 Other;
```

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Alignment Scores:
Pred.No.: 6e-56 Length: 969
Score: 992.50 Matches: 195
Percent Similarity: 83.78% Conservative: 22
Best Local Similarity: 75.29% Mismatches: 39
Query Match: 57.54% Indels: 3
DB: 4 Gaps: 2
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US-10-089-278-6 (1-329) x AAF30730 (1-969)
Qy 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnGlnSerGlyAlaGluLeuValArg 60
Db 46 GCGGCCAGCCGGCCCATGGCGAGGTTTCAGCTTCAGCAGCTCGAGCTGGTGAAG 105
Qy 61 ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
Db 106 CCGGGGCTCAGTGAAGATTCTCTGCAAAAGCTTCCTGGCTACGCATTCAGTACTCTGG 165
Qy 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
Db 166 ATGAACCTGGGTGAAGCAGAGCCCTGGACAGGGTCTTGAGTGGATTGGACGGATTATCCT 225
Qy 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db 226 GGAATGGAGATACATAACTACATGGAAGTTCAAGGGCAAGGCCACACTGACTGCAGAC 285
Qy 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db 286 AATCTCTCCAGCAGACCTACATGAGCTCAGCAGCTGACCTCTCTGGACTCTGCGGTC 345
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QY 141 TTTTCTGTGCA-----GATGTAAGTA---TATTACTATGCTATGACTACTGGGT 396
Db 161 GlnGlyThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 180
QY 397 CAAGGAACCTCAGTCCAGCTCTCTCAGGTGGAGCGGTTTCAGTGGCGCGCTCTGGC 456
Db 181 GlyGlyGlySerAspThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 200
QY 457 GGTGGCGGATCGCAAAATGTTCTCACCCAGTCTCTCTCTCTCTCTCTCTCTCTCT 516
Db 201 GlnArgAlaThrIleSerCysArgAlaSerGlnSerValAspSerTyrGlyAspSerPhe 220
QY 517 CAGAGGGCCACCATCTCATGCGGGCCAGCAAGATGTCAGTACATCTGGCTATAGTTAT 576
Db 221 MetHisTrpTyrGlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArgAlaSer 240
QY 577 ATGCACTGGTACCAACAGAAACCAGACAGCCACCCCAAACTCTCATCTATCTTGCATCC 636
Db 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGlySerGluSerPheThr 260
QY 637 AACCTAGAATCTGGGTCCCTCCAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACC 696
Db 261 LeuThrIleAspProValGluGluAspAspAlaAlaValTyrTyrCysLeuGlnSerMet 280
QY 697 CTCACATCATCTCTGTGGAGGAGGAGTCTGCAACCTATTACTTGTTCAGCACATAGG 756
Db 281 GluAspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAla 299
QY 757 GAGCTTCCTCGGACGTTCTGGTGGAGGAGGAGTCTGCAACCTATTACTTGTTCAGCACATAGG 813
Db 757 GAGCTTCCTCGGACGTTCTGGTGGAGGAGGAGTCTGCAACCTATTACTTGTTCAGCACATAGG 813

RESULT 12
AD588776
ID ADS88776 standard; DNA; 897 BP.
XX
AC ADS88776;
XX
XX
DT 16-DEC-2004 (first entry)
XX
DE Nucleotide sequence of the IC2 scFv antibody from clone p530.
XX
KW G glycoprotein; respiratory syncytial virus;
KW respiratory syncytial virus infection; RSV; RSV infection; IC2; scFv;
KW gene; ds.
XX
OS Mus sp.
XX Synthetic.
XX
PH Key
FT CDS
FT 1..897
FT Location/Qualifiers
FT /*tag= b
FT /product= "IC2 scFv"
FT sig_peptide
FT 1..66
FT /*tag= a
FT /note= "PelB leader sequence"
FT
FN WO2004083373-A2.
XX
XX 30-SEP-2004.
XX
XX 22-MAR-2004; 2004WO-GB001239.
XX
XX 22-MAR-2003; 2003GB-00006618.
XX (UYNE-) UNIV NEWCASTLE-UPON-TYNE.
XX
XX Toms G, Routledge E, Mekseepalard C;
XX WPI; 2004-691033/67.
XX P-PSDB; ADS88777.
XX

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PT New antibody against the G glycoprotein of RSV with a variable region
PT having a first and second domain from a VL and VH region, respectively,
PT useful for treating respiratory syncytial virus (RSV) infections.
XX
PS Example 2; SEQ ID NO 44; 93pp; English.
XX
CC The specification describes an against the G glycoprotein of respiratory
CC syncytial virus, with a variable region comprising a first domain from a
CC variable light chain region and a second domain a variable heavy chain
CC region. The antibodies of the invention are useful for treating and
CC preventing the development of infections caused by the respiratory
CC syncytial virus (RSV). The present sequence encodes the IC2 scFv from
CC clone p530. This scFv is an exemplary antibody of the invention. IC2 is a
CC murine monoclonal antibody known to bind to the SV G glycoprotein. IC2
CC was used as a source of sequences to construct antibodies of the
CC invention.
XX
SQ Sequence 897 BP; 224 A; 215 C; 251 G; 207 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6,97e-56 Length: 897
Score: 991.00 Matches: 191
Percent Similarity: 83.85% Conservative: 27
Best Local Similarity: 73.46% Mismatches: 40
Query Match: 57.45% Indels: 2
DB: 13 Gaps: 2
US-10-089-278-6 (1-329) x ADS88776 (1-897)
QY 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg 60
Db 46 GCGGCCACGCCGCCATGGCCAGGTGTCAGTGCAGCAGTCAGGGCTCAGGTGGTGGAG 105
QY 61 ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
Db 106 CCTGGGGTCTCAGCGAGGATTTCTGCAAGGGATTCGGCTACACATTCAGTATTAGCT 165
QY 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
Db 166 ATGCACTGGTGAAGCAGAGTCACGCCAAGAGTCTAGAGTGGATTGGAGTTATTAGTACT 225
QY 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db 226 TACTATGTTAATCCAAATTAACAACCAAGAGTTTAAAGGCAAGGCCACAATAGCTGTAGAC 285
QY 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db 286 AAATCCTCCAGCACAGCCTATATGGAACCTTGCCAGATTGACATATGAGGATTCGCCATC 345
QY 141 TyrTyrCysAlaArgSerAspGly---AsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrp 159
Db 346 TATTACTGTGCAAGATCGGTATGATTACGGCCGGCGGGGTATGCTATGGACTACTGG 405
QY 160 GlyGlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlySer 179
Db 406 GGCACAGGACACACGGTCCAGCTCTCGAGTGGTGGAGCGGGTTTCAGCGGAGGTGGCTCT 465
QY 180 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeu 199
Db 466 GCGGTAGTGGCACAGGATGTTTGTGATGCCAGACTCCTCTCTCTCTCTCTCTCTCTCT 525
QY 200 GlyGlnArgAlaThrIleSerCysArgAlaSerGluSer---ValAspSerTyrGlyAsp 218
Db 526 GGAGATCAAGCCCTCCATCTCTTGCAGATCTAGTCAGAACATTGTATAGTATGGAAC 585
QY 219 SerPheMetHisTrpTyrGlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArg 238
Db 586 ACCTATTAGAGTGGTACCTTCAGAGAACACAGGCCAGTCTCCAAAGCTCTCTGATCTACAA 645
QY 239 AlaSerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAsp 258
Db 646 GTTTCACACCGATTTTCTGGGGTCCACAGACAGGTTTCAGTGGCAGTGGATCGGACAGAT 705

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QY 259 PheThrLeuThrIleAspProValGluGluAspAlaAlaValTyrCysLeuGln 278
DB 706 TTCACACTCAAGATCAGCAGTGGAGCTGGAGTCTGGAGTTTATTACTGCTTCAA 765

QY 279 SerMetGluAspProTyrThrPheGlyGlyThrLysLeuGluLeuLysArgAlaAla 298
DB 766 GGTTCACATATTCGTGGACGTTGGTGGAGGACCAAGCTGGAGATCTCCGGCGCGCA 825

RESULT 13
AAZ43431
ID AAZ43431 standard; DNA; 1698 BP.
XX
AC AAZ43431;
DT 18-FEB-2000 (first entry)
XX
DE Fv-antibody construct containing antibody 9E10 epitope DNA.
XX
KW Multivalent; Fv-antibody; antiviral; antibacterial; cytostatic;
KW diagnosis; therapy; disease; ss.
XX
OS Synthetic.
XX
PN DE19819846-A1.
XX
XX 11-NOV-1999.
XX
XX 05-MAY-1998; 98DE-01019846.
XX
XX 05-MAY-1998; 98DE-01019846.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX Little M, Kipriyanov S;
XX
XX WPI; 2000-024472/03.
XX
XX P-PSDB; AAY50822.
XX
XX Multivalent Fv-antibody constructs with at least four variable domains
XX connected by 1, 2 and 3 peptide linkers.
XX
XX Example 1; Fig 5; 14pp; German.
XX
XX This invention describes a novel multivalent Fv-antibody construct with
XX at least four variable domains that are connected to one another by 1, 2
XX and 3 peptide linkers. The construct has antiviral, antibacterial and
XX cytostatic activity. The multivalent Fv-antibody constructs are useful
XX for the diagnosis and/or therapy of disease, especially viral, bacterial
XX or tumor diseases. The multivalent Fv-antibody constructs have increased
XX stability when in the form of a single chain dimer. This sequence encodes
XX a bivalent Fv antibody construct composed of the antibody 9E10 epitope in
XX expression plasmid pDISC3x19-L1.
XX
SQ Sequence 1698 BP; 433 A; 434 C; 450 G; 381 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 13e-55 Length: 1698
Score: 991.00 Matches: 197
Percent Similarity: 80.50% Conservative: 30
Best Local Similarity: 69.86% Mismatches: 45
Query Match: 57.45% Indels: 10
DB: 3 Gaps: 3

US-10-089-278-6 (1-329) x AAZ43431 (1-1698)

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DB 73 GCAGCTCAGCGCCATGGCGCAGGTGCACACTGCAGCAGTCTGGGCTGAACTGGCAAGA 132

QY 61 ProGlyValSerValLysLeuSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
DB 133 CTGGGGCCTCAGTGAAGATGTCTGCAAGGCTTCTGGCTACACCTTTTACTAGGTACAG 192

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QY 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGlnTrpIleGlyLeuIleSerThr 100
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QY 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
DB 253 AGCGTGGTTTATCTAATTACATCAGAACTTCAAGGACAAGGCCACATTGACTACAGAC 312

QY 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
DB 313 AAATCCTCCAGCAGCAGCTACATGCACTGAGCAGCCTGCATCTGAGGACTCTGCAGTC 372

QY 141 TyrTyrCysAlaAlaArgSerAspGlyAsnTyrGlyTyrTyrAlaLeuAspTyrTrpGly 160
DB 373 TATTACTGTGCAAGA-----TATTATGATGATCAITTACAGCCTTGACTCTGGGGC 423

QY 161 GlnGlyThrThrValThrValSerSerGlyGlyGlyLysSerGlyGlyGlySerGly 180
DB 424 CRAAGGCACCACTCTCAGAGTCTCTCAGCCAAACAACACCCCAAGCTTGGCGGT----- 477

QY 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200
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QY 201 GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220
DB 526 CAGAGGGCCACCATCTCTCGAAGGCCAGCCAAACTCCCTCATCTATGATGATGATTAT 585

QY 221 MetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSer 240
DB 586 TTGAACCTGGTACCACAGATTCAGGACAGCCACCCAACTCCCTCATCTATGATGATGAT 645

QY 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260
DB 646 AATCTAGTTTCTGGGATCCACCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACC 705

QY 261 LeuThrIleAspProValGluGluAspAspAlaAlaValTyrTyrCysLeuGlnSerMet 280
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QY 281 GluAspProTyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAlaAsp 300
DB 766 GAGGATCCGTGGAGCTTCCGTGGAGGCCACCAAGCTGAAATCAACCGGCTGATGCTGCG 825

QY 301 GlySerGlyGlyGlyGlySer---GlyGlyGlySerGlyGlyGlySerGlyGlyGly 319
DB 826 GCGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 885

QY 320 GlySer 321
DB 886 GGTAGC 891

RESULT 14
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AC AAZ44206;
DT 31-MAR-2000 (first entry)
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DE Murine derived DNA fragment #4.
XX
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KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KW HIV infection; autoimmune disease; murine; ds.
XX
OS Mus sp.
XX
XX WO9961629-A1.
XX
XX 02-DEC-1999.
XX
XX 24-MAY-1999; 99WO-JP002711.

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Qy 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db 226 GGAAGTGGTAGTCTTACTACATGAGATGTTCAAGGGCAAGGCCACACTGACTGCAGAC 285
Qy 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db 286 AATCCTCCAAACAGACCTACATGCTCAGCAGCCTGACATCTGAGGACTCTGGCGTC 345
Qy 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrAlaLeuAspTyrTrpGly 160
Db 346 TATTTCGTGCAAGACCGGAACCTGGGACGGGGTTT-----GCTTACTGGGGC 393
Qy 161 GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 180
Db 394 CGAGGGACTCTGGTCACTGCTCTGCAAGTGGAGCGGTTCAAGCGGAGGTGGCTCCGA 453
Qy 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200
Db 454 GGTGGCGGATCGGACATTGTGCTGACCCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGG 513
Qy 201 GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220
Db 514 CAGAGGCCCAACCATCTCTCGAAGCCAGCCAAAGTGTGATTATGATGGTGATGTTAT 573
Qy 221 MetHisTrpTyrGlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArgAlaSer 240
Db 574 ATGAACCTGGTACCAACAGAACCCAGGACGCCCAAACTCCTCATCTATGCTGCATCC 633
Qy 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260
Db 634 AATCTAGAATCTGGATCCCGAGCCAGGCTTTAGTGGCAGTGGTCTGGGACAGACTTCACC 693
Qy 261 LeuThrIleAspProValGluAspAspAlaAlaValTyrTyrCysLeuGlnSerMet 280
Db 694 CTCAACTCCATCCTGTGGAGGAGGAGGATGCTGCACCTATTACTGTCTCAGCAAGTAGT 753
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Search completed: August 23, 2005, 14:42:30
Job time : 548 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 23, 2005, 13:50:35 ; Search time 3106 Seconds

(without alignment)
4031.920 Million cell updates/sec

Title: US-10-089-278-6

Perfect score: 1725

Sequence: 1 MDCLTNLSAEKGVQASKI.....GSGGGSGGGSGASPVQFI 329

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10089278@cgn 1_1_5180 @runat 23082005 121734 29344 -NCPU=6 -ICPU=3
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gest1.*
9: gb_gest2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	761	44.1	671	3 AF240168	AF240168 Mus muscu
C 2	671	38.9	872	7 CK629396	CK629396 AMO-AA001
C 3	668	38.7	601	5 BQ474958	BQ474958 carabus4g
C 4	645	37.4	1104	7 CK629846	CK629846 AM2-AA002
C 5	638	37.0	1339	7 CK629414	CK629414 AM1-AA001
6	631.5	36.6	672	7 CK633068	CK633068 AM3-AP001
7	631.5	36.6	672	7 CK633069	CK633069 AM3-AP001
C 8	631	36.6	535	3 AF240170	AF240170 Mus muscu
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C 10	629.5	36.5	1419	7	CK629415	CK629415 AM1-AA001
C 11	602	34.9	823	7	CK632348	CK632348 AMO-AM000
C 12	599	34.7	683	3	AF240172	AF240172 Mus muscu
C 13	523	30.3	407	2	AW988429	AW988429 ug08d07.Y
14	520.5	30.2	565	2	BF801321	BF801321 MRO-CI002
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16	510	29.6	327	4	BG148320	BG148320 uu91c06.Y
C 17	505.5	29.3	567	5	BQ328142	BQ328142 MR4-RT004
C 18	505.5	29.3	963	7	CK629843	CK629843 AM2-AA002
C 19	503.5	29.2	489	2	BF855922	BF855922 PM2-FN021
20	503	29.2	544	5	BQ310337	BQ310337 MRO-BT450
21	500	29.0	732	4	BG962768	BG962768 602830291
22	498	28.9	750	4	BG965050	BG965050 602829112
23	498	28.9	876	4	BI107286	BI107286 602894285
24	492.5	28.6	453	5	BQ346956	BQ346956 PM2-NT016
25	489.5	28.4	504	2	BF759134	BF759134 MRO-CT054
26	489.5	28.4	577	1	AJ548139	AJ548139 AJ548139
27	486.5	28.2	569	2	BF842604	BF842604 MRO-HT092
28	483.5	28.0	527	2	BF921283	BF921283 PM2-NT016
29	478.5	27.7	626	7	CK632177	CK632177 AM1-AM000
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31	475	27.5	599	5	BQ310276	BQ310276 MRO-BT250
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33	469	27.2	922	2	BF584560	BF584560 602098269
34	468.5	27.2	507	2	BF015548	BF015548 uy23a08.Y
C 35	468	27.1	585	4	BI030095	BI030095 IL0-MT035
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42	460	26.7	806	4	BI108506	BI108506 602894952
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45	457	26.5	926	2	BF787780	BF787780 602113542

ALIGNMENTS

RESULT 1	LOCUS	AF240168	Mus musculus MRP5 mRNA, partial cds.	671 bp	mRNA	linear	HTC	30-APR-2001
AF240168	DEFINITION	Mus musculus MRP5 mRNA, partial cds.						
AF240168	ACCESSION	AF240168						
AF240168.1	VERSION	AF240168.1	GI:13877288					
HTC	KEYWORDS	HTC						
Mus musculus (house mouse)	SOURCE	Mus musculus						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	ORGANISM	Mus musculus						
Cui, D.X., Zeng, G.Y., Wang, F., Xu, J.R., Ren, D.Q., Guo, Y.H., Tian, F.R., Yan, X.J., Hou, Y., and Su, C.Z.	REFERENCE	1 (bases 1 to 671)						
Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after gamma-irradiation in mice	AUTHORS	World J. Gastroenterol. 6 (5), 709-717 (2000)						
11819679	JOURNAL	2 (bases 1 to 671)						
Cui, D., Zeng, G., Yan, X., Li, X. and Su, C.	REFERENCE	2 (bases 1 to 671)						
Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain	AUTHORS	Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19 (1), 71-80 (2001)						
3 (bases 1 to 671)	JOURNAL	3 (bases 1 to 671)						
Cui, D., Zeng, G., Yan, X., Wang, F., Tian, F., Ren, D., Zhao, T., Li, X. and Su, C.	REFERENCE	3 (bases 1 to 671)						
Direct Submission	AUTHORS	Submitted (02-MAR-2000) Molecular Cloning Laboratory, Institute of Genetic Diagnosis, Fourth Military Medical University, No. 17 Chang Le West Road, Xi'an 710032, China						
Location/Qualifiers	TITLE							

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Alignment Scores:
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Query Match: 44.12% Indels: 4
DB: 3 Gaps: 1

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DEFINITION
sequence.
VERSION CK629396.1 GI:45753871
KEYWORDS Apis mellifera (honey bee)
SOURCE Apis mellifera
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apidae; Apis.
REFERENCE 1 (bases 1 to 872)
Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espreatico,E.M.,
Espindola,F.S., Pado-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
Silva,W.A. Jr.
Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
Unpublished (2004)
JOURNAL Contact: Silva Jr, W. A.
COMMENT Molecular Genetic and Bioinformatics Laboratory
Department of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Caiao Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonj@usp.br
This sequence was derived from the FAPESP Genome Program
High quality sequence start: 66
High quality sequence stop: 625.
FEATURES
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Query Match: 38.90% Indels: 15
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Qy 85 LysGlnSerHisAlaLysSerLeuTrpIleGlyLeuLeuSerThrTyrTyrGlyAsp 104
Db 717 AGGCAGACGCTGAACAGGACTTTCAGTGGATGGATG-CTTTTCTCGGAGGGGAGT 659
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Qy      283  ProTyrThrPheGlyGlyThrLysLeuGluIleLysArgAla 297
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RESULT 3
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AUTHORS
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MEDLINE
PUBMED
COMMENT
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source

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BQ474958
GI:25957232
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Carabus granulatus
Carabus granulatus
Carabus granulatus
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Carabina; Carabus; Carabus.
Theodorides,K., de Riva,A., Gomez-Zurita,J., Foster,P.G. and
Vogler,A.P.
Comparison of EST libraries from seven beetle species: towards a
framework for phylogenomics of the Coleoptera
Insect Mol. Biol. 11 (5), 467-475 (2003)
22217875
12230545
Contact: Foster PG
Vogler, Entomology
The Natural History Museum
Cromwell Road, London, SW7 5BD
Email: p.foster@nhm.ac.uk.
Location/Qualifiers
1. 601
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/mol_type="mRNA"
/db_xref="taxon:118799"
/clone="carabus4g12"
/cdna_lib="Carabus granulatus cDNA"
/note="Vector: pUC18"

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ORIGIN
Alignment Scores:
Pred. No.: 4,39e-52 Length: 601
Score: 668.00 Matches: 129
Percent Similarity: 75.71% Conservative: 30
Best Local Similarity: 61.43% Mismatches: 39
Query Match: 38.72% Indels: 12
DB: 5 Gaps: 3

US-10-089-278-6 (1-329) x BQ474958 (1-601)
Qy      90  LysSerLeuGluTrrPheGlyLeuIleSerThrTyrTyrGlyAspProSerTyrAsnGln 109
Db      601  CAGGAGCTTGAAGTGGATGGATGGATTTTCTCGAGAGGGAGTACTGAATACATATGAG 542
Qy      110  ArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyrLeuGlu 129
Db      541  AAGTTCAAGGGCAGGGCCACACTGAGTGTAGACAGTCTCTCCAGCACACCTATATGGAG 482
Qy      130  LeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAspGlyAsn 149
Db      481  CTCACCTAGGCTGACATCTGAGGACTCTGCTGTCTATTCTGTCTAGAGGGGAC----- 428
Qy      150  TyrGlyTyrTyrTyrAla-----LeuAspTyrTrrPheGlyGlnGlyThrThrValThrVal 167
Db      427  -----TACTATAGGCGGTACTTTGACTTTGTGGGGCCAAAGGGACCAAGGTCAACGTC 377
Qy      168  SerSerGlyGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGlyGlyGlyGly 187
Db      376  TCCTCATGTGGAGGCGGTTTCAGGCGGAGGTGGCTCTGGCGGTGGCGATCTGCATTTGAG 317
Qy      188  LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
Db      316  CTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTACCACATGACCTGC 257
Qy      208  ArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTrrPyrGlnGlnLys 227
Db      256  AGTGCAGCTCAAGTATA-----CGTTACATATATTGGTACCACAGAG 212
Qy      228  ProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGlyValPro 247
Db      211  CTTGGATCTCTCCCGCAGACTCTCTGATTTATGACATCCACGCTGGCTCTCTGGAGTCCCT 152
Qy      248  AlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspProValGlu 267
Db      151  TTTCCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTATTCTCTCAATCAACCGAATGGAG 92
Qy      268  GluAspAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGly 287
Db      91  GCTGAGGATGCTGCCACTTATTACTGCCAGGAGTGGAGTGGTTATCCGTACACGTTCCGA 32
Qy      288  GlyGlyThrLysLeuGluIleLysArgAla 297
Db      31  GGGGGGACCAAGCTGGAGCTGAACGGGGC 2

RESULT 4
BQ629846/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

BQ629846
1104 bp mRNA linear EST 26-MAR-2004
AM2-AA0023-091202-021-F02 AA0023 Apis mellifera cDNA, mRNA
sequence.
BQ629846
CK629846.1 GI:45754321
EST.
Apis mellifera (honey bee)
Apis mellifera
Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apidae; Apis.
1 (bases 1 to 1104)
Nunes,P.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Mata,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,

```


/note="MRP7; transcript related to the repair of irradiation-damaged intestinal gland cells treated with RNA; coding region not determined"

ORIGIN

Alignment Scores:

Pred. No.:	1.06e-48	Length:	535
Score:	631.00	Matches:	127
Percent Similarity:	81.8%	Conservative:	17
Best Local Similarity:	72.1%	Mismatches:	23
Query Match:	36.5%	Indels:	10
DB:	3	Gaps:	2

US-10-089-278-6 (1-329) X AF240170 (1-535)

Qy	41	Ala	Ala	Gln	Pro	Ala	Met	Ala	Glu	Val	Leu	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	60	
Db	534	CGG	CGC	CAG	CGG	CGC	ATG	GGC	CAG	CGT	AAA	CTG	CAG	CAG	T	CAG	GCT	GAG	TGG	TGAG	475
Qy	61	Pro	Gly	Val	Ser	Val	Ile	Ser	Cys	Ala	Gly	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	Gly	80
Db	474	CTG	GGG	GCT	CAG	TGA	AGATT	TCT	GCA	AGG	TTT	CGG	CTC	ACA	CA	TTC	ACT	GAT	TAT	TCT	415
Qy	81	Met	Ser	Trp	Val	Lys	Gln	Ser	His	Ala	Lys	Ser	Leu	Glu	Trp	Ile	Gly	Leu	Ile	Ser	100
Db	414	ATG	CACT	GGCT	GAG	ATG	CAAT	CA	TG	CA	CAG	AGT	CT	GAG	TGG	AGT	TGG	AAT	TAT	TAT	355
Qy	101	Tyr	Tyr	Gly	Asp	Pro	Ser	Tyr	Asn	Gln	Arg	Phe	Lys	Gly	Lys	Ala	Thr	Met	Thr	Val	120
Db	354	TAC	GAT	GTA	TAA	TACA	AACT	ACA	CA	CAG	AGT	TTT	TAA	GCG	CAAG	CCCA	TAT	GACT	GTT	TGAC	295
Qy	121	Lys	Ser	Ser	Asn	Thr	Ala	Tyr	Leu	Glu	Leu	Ala	Arg	Leu	Thr	Ser	Glu	Asp	Ser	Ala	140
Db	294	AAAT	CTC	CAAT	TAC	AGC	TAT	ATG	AACT	TTG	CC	AGAT	TG	CA	CT	GAT	GAT	TCT	GC	CAAT	235
Qy	141	Tyr	Tyr	Cys	Ala	Arg	Ser	Asp	Gly	Asn	Tyr	Gly	Tyr	Tyr	Trp	Ala	Leu	Asp	Tyr	Trp	160
Db	234	TATT	ACT	GTG	CAA	GAGG	---GCT	TACT	AC	GCG	TAG	TTT	TATT	TACT	TTT	TACT	ACT	TGG	GGC	178	
Qy	161	Gln	Gly	Thr	Thr	Val	Ser	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	180
Db	177	CAAG	GAC	CCG	GTC	ACG	GTC	CTC	T	CAG	TGG	AGG	CGG	TT	CAG	CGG	AGG	TGG	CT	CTGGC	118
Qy	181	Gly	Gly	Ser	Asp	Ile	Glu	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ala	Val	Ser	Leu	Gly	200
Db	117	GGT	GCG	ATC	GGA	---ATC	GAG	CTC	ACC	CAG	GGG	GGC	ACC	CA	AGCT	TGG	AAAT	CAAA	CGG	CGCG	59
Qy	201	Gln	Arg	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	208
Db	58	CGC	AGG	TG	CGC	GGT	CGCG	TAT	CCG	AT	TCG	CT	CGG	AA	CCG	CGT	CGG	AA	CCG	CGT	11

RESULT 9			
AF240167	LOCUS	AP240167	540 bp mRNA
DEFINITION	Mus musculus MRP4	complete cds.	linear
			HTC 30-APR-2001

AF240167

VERSION AF240167.1 GI:13877286
KEYWORDS: UMC

KEYWORDS

SOURCE	Mus musculus (house mouse)
OPCANTISM	Mus musculus

ORGANISM MUS MUSCULUS
Eukaryota: Mammalia: Mus musculus

REFERENCE
1 (bases 1 to 540)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi
Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi

AUTHORS
Cui, D. X., Zeng, G. Y., Wang, F., Xu, J. B.,

Tian, F.R., Yan, X.J., Hou, Y. and Su, C.Z.

TITLE Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after gamma-irradiation in mice

JOURNAL World J. Gastroenterol. 6 (5), 709-717 (2000)

PUBMED 11819679

REFERENCE 2 (bases 1 to 540)

AUTHORS Cui, D., Zeng, G., Yan, X., Li, X. and Su, C.

TITLE Cloning of mouse genes related to repairing of intestinal

epithelium of the irradiated mice by treatment with the intestinal

JOURNAL

REFERENCE
AUTHORS

TITLE
JOURNAL.

FEATURES

CDS

ORIGIN

Alignment Scores:

Length:	1.07e-48	540
Matches:	631.00	127
Conservative:	81.82%	17
Mismatches:	72.16%	23
Indels:	36.58%	10
Gaps:		2
DB:		3

US-10-089-278-6 (1-329) x AF240167 (1-540)

41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnGlnSerGlyAlaGluLeuValArg 60
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9 GCGGCCACCGGGCCATGGCCCGAGGTGAACTGCAGCAGCTCAGGACCTGAGGTGGTGAGG 68
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61 ProGlyValSerValIysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
69 CCTGGGCTCAGTGAGATTTCTCGAAGGGTTCGGGCTACACATTCAGTATTCT 120

81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 10
129 ATGCATCGCTGAAGATGAATCATGCACAGAGCTTAGAGTGGATTGGAATTATTAGTACT 18

101 TyrTyrGlyAspProSerTyrAsnGlnAArgPheLysGlyLysAlaThrMetThrValAsp 12
||| : : : : : : : : : : : : : : : : : :
189 TACGATGGTAATACAACACTACAACCAGAAGTTTAAAGGGCAAGGCCACTATGACTGTGGAC 24

121 LysSerSerAsnThrAlaTyrIeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle
249 AAATCCTCCATTACAGCCTATATGGAACCTGCCAGATTGACATCTGATGATTCGTGCCATC

141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGly
 309 TATTACTGTGCAAGAGGG---GCTTACTACGGTAGTTTTTTATTACTTTGACTACTGGGCG

161 GlnGlyThrThrValSerSerGlyGlyGlySerGlyGlyGlyGlySerGly 18

366 CAAGGGACCA CGGTACC GTCTCTC AGGTGGAGCGGTT CAGGC GGAGGTG CTCTGC 42

181 GlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeucly 20

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Db      426 GGTGGCGGATCGGA-ATCGAGCTCACCAGGGGGCACCAAGCTGGAATCAACAGGGCGGC 484
Qy      201 GlnArg-----AlaThrIleSerCysArg 208
Db      485 GCGAGGTGCGCGGTGCGGTATCCGGATCCCGCTGGAAACCGGTGCCGC 532

RESULT 10
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LOCUS   CK629415      1419 bp      mRNA      linear      EST 26-MAR-2004
DEFINITION AM1-AA0014-041102-021-H09 AA0014 Apis mellifera cDNA, mRNA
VERSION   CK629415
KEYWORDS  EST.
SOURCE    CK629415.1 GI:45753890
ORGANISM  Apis mellifera (honey bee)

REFERENCE
1 (bases 1 to 1419)
Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espreatico,E.M.,
Espindola,F.S., Paco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
Silva,W.A. Jr.

Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
Unpublished (2004)
Contact: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Department of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catão Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br
This sequence was derived from the FAPESP Genome Program
High quality sequence start: 63
High quality sequence stop: 605.
Location/Qualifiers
1..1419
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/strain="Africanized"
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/sex="female, worker"
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/clone_lib="AA0014"
/note="Organ: whole body"

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Percent Similarity: 72.32%      Conservative: 31
Best Local Similarity: 58.48%      Mismatches: 50
Query Match:     26.49%      Indels:     15
DB:              7          Gaps:        3

US-10-089-278-6 (1-329) x CK629415 (1-1419)

Qy      75 ThrPheThrAspTyrGlyMetSerTrpVallyGlnSerHisAlaLysSerLeuGluTrp 94
Db      728 ACATTCACAGTATGATATAGACTGGTG-AGCAGAGCC- TGNACAGGACTTTGAGTGG 671

Qy      95 IleGlyLeuIleSerThrTyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLys 114
Db      670 ATTGGATC-ATTTTCTCGGAGGAGGANGTACTGAATACATAGAACTCAAGGGCCAGG 612

Qy      115 AlaThrMetThrValAspLysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThr 134
Db      611 CACACACTGATGTAGACAAGTCTCCAGCACAGCCTATATGGAGCTCACTAGGCTGACA 552

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Qy      135 SerGluAspSerAlaIleTyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyr 154
Db      551 TCTGAGGACTCTGCTCTATTCTGTGCTAGAGGGGAC-----TACTAT 507

Qy      155 Ala-----LeuAspTyrTrpGlyGlnGlyThrValThrValSerSerGlyGlyGly 172
Db      506 AGCGCGCTACTTTGACTTTGTGGGCCAAGGGACCAACGCTCACCGTCTCTCATGTGGAGAC 447

Qy      173 GlySerGlyGlyGlySerGlyGlyGlyGlySerAspIleGluLeuThrGlnSerPro 192
Db      446 GGTTCAGCGGAGGTGCTCTGCGGTGGCGGATCTGACATTGAGCTCACCCAGTCTCCA 387

Qy      193 SerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCysArgAlaSerGluSer 212
Db      386 GCATCATGCTGCTCACTCTCCAGGGGAGAGGGTCCACCATGACCTGCAGTGCAGCTCAAGT 327

Qy      213 ValAspSerTyrGlyAspSerPheMetHisTyrTrpGlnGlnLysProGlyGlnProPro 232
Db      326 ATA-----CGTTACATATATTGGTATCCACAGAACGCTGGATCCTCCTCC 282

Qy      233 LysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGlyValProAlaArgPheSerGly 252
Db      281 AGACTCTCTGATTATATGACATCCACAGTGGCTCTCGAGTCCCTTTTCCGCTTCAGTGGC 222

Qy      253 SerGlySerGluSerAspPheThrLeuThrIleAspProValGluGluAspAlaAla 272
Db      221 AGTGGGTCTGGGACCTCTTATTCTTCACAAATCAACGAATGAGGCTGAGGATGCTGCC 162

Qy      273 ValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGlyGlyGlyThrLysLeu 292
Db      161 ACTTATTACTGCCAGGAGTGGAGTGTCTTATCCGTACACGTTTCGAGGGGGGACCAAGCTG 102

Qy      293 GluIleLysArg 296
Db      101 GAGCTGAACGC 90

RESULT 11
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LOCUS   CK632348      823 bp      mRNA      linear      EST 26-MAR-2004
DEFINITION AM0-AM0009-070103-021-H02 AM0009 Apis mellifera cDNA, mRNA
VERSION   CK632348
KEYWORDS  EST.
SOURCE    CK632348.1 GI:45756823
ORGANISM  Apis mellifera (honey bee)

REFERENCE
1 (bases 1 to 823)
Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espreatico,E.M.,
Espindola,F.S., Paco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
Silva,W.A. Jr.

Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
Unpublished (2004)
Contact: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Department of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catão Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br
This sequence was derived from the FAPESP Genome Program
High quality sequence start: 70
High quality sequence stop: 545.
Location/Qualifiers
1..823

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FEATURES
source

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/organism="Apis mellifera"
/mol_type="mRNA"
/strain="Africanized"
/db_xref="taxon:7460"
/sex="female, worker"
/dev_stages="Mix of adult, pupal, larval and embryonic."
/clone_lib="AM0009"
/note="Organ: whole body"

ORIGIN
Alignment Scores:
Pred. No.: 9,46e-46 Length: 823
Score: 602.00 Matches: 128
Percent Similarity: 66.01% Conservative: 39
Best Local Similarity: 50.59% Mismatches: 64
Query Match: 34.90% Indels: 22
DB: 7 Gaps: 5

US-10-089-278-6 (1-329) x CK632348 (1-823)
QY 43 GlnProAlaMetAlaGluValIysLeuGlnSerGlyAlaGluLeuValArgProGly 62
Db 87 CAGCGGGGATGGCCAGGTAAGCTGCAGAGTGAAGGAACTGAAGTGGTAAGACCTGGG 146
QY 63 ValSerValIysIleSerCysLeuGlySerGlyTyrThrPheThrAspTyrGlyMetSer 82
Db 147 GCTTCAGTGAAGTTGCTCGAGAGCTTCGGCTACATCTTCACAGTTATGATATAGAC 206
QY 83 TrpValIysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyr 102
Db 207 TGGGTGAGGCAGACCGCTCAACAGCACTTGAGTGGCTTGGATGATTTTCTCTGGAGAG 266
QY 103 GlyAspProSerTyrAnGlnArgPheIysGlyIysAlaThrMetThrValAspLysSer 122
Db 267 GGGAGTACTCAATCAATAGAGTTCAAGGCGGACCTGAGTGTAGACAGTCC 326
QY 123 SerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyr 142
Db 327 TCAGACAGCCTATATGAGGCTCAGTGGCTGACATCTGAGGACTCTGCTGCTATTTTC 386
QY 143 CysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAla-----LeuAspTyrTrpGly 160
Db 387 TGTGCTAGAGGGAC-----TACTATAGGCGCTACTTTGACTTGTGGGC 431
QY 161 GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 180
Db 432 CAAGGGACCAACGCTCCTCATGTGAAGCGGTTTCAAGCGGAGGCTCTGGC 491
QY 181 GlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAla--ValSerLeuG 200
Db 492 GGTGGCGGATCTGACATGTAGCTCACCAGTCTCCAGCATCATGTCTGCATCTCCAGTG 551
QY 200 lyGlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerP 220
Db 552 GAAGAGGTCACCAATGACCTGAGTGCAGTCAAGCTCAAGTATA-----CGTN 596
QY 220 heMetHisTrpTyrGlnGlnIysProGlyGlnProIysLeuLeuIle-----T 237
Db 597 ACATATATTGGTTTCAACAGAGCGCTGGATCCTCCCGCCAGCATCTGATATGACACATC 656
QY 237 YrArgAlaSerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluS 257
Db 657 AAGTGGCCCTGGAGTCTTTCG-----CTCAGTGGCAGTGGTCTGGACC 701
QY 257 erAspPheThrLeuThrIleAspProValGluGluAspAlaAlaValTyrTyrCysL 277
Db 702 TCTTATTCTCTCAAAATCACCAGTGGAGCTGAGATCTGATATATGCTGCGGAGTGATGA 761
QY 277 euGlnSerMetGluAspProTyrThrPheGlyGly 288
Db 762 TCCGACCTTCGGAGGGACCACTGAGCGAAGGGGC 796

RESULT 12
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AF240172/c
LOCUS AF240172 683 bp mRNA linear HTC 30-APR-2001
DEFINITION Mus musculus MRP9 mRNA, partial cds.
ACCESSION AF240172
VERSION AF240172.1 GI:13877293
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Sukariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 683)
Cui,D.X., Zeng,G.Y., Wang,F., Xu,J.R., Ren,D.Q., Guo,Y.H.,
Tian,F.R., Yan,X.J., Hou,Y. and Su,C.Z.
Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after gamma-irradiation in mice
World J. Gastroenterol. 6 (5), 709-717 (2000)
11819679
2 (bases 1 to 683)
Cui,D., Zeng,G., Yan,X., Li,X. and Su,C.
Cloning of mouse genes related to repairing of intestinal
epithelium of the irradiated mice by treatment with the intestinal
RNA of mice of the same strain
Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19 (1), 71-80
(2001)
3 (bases 1 to 683)
Cui,D., Zeng,G., Yan,X., Wang,F., Tian,F., Ren,D., Zhao,T., Li,X.
and Su,C.
Direct Submission
Submitted (02-MAR-2000) Molecular Cloning Laboratory, Institute of
Genetic Diagnosis, Fourth Military Medical University, No. 17 Chang
Le West Road, Xi'an 710032, China
Location/Qualifiers
1. 683
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/sex="male"
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/notes="derived from differential display PCR between
irradiated mice with and without RNA injection"
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/translation="LCGTRFQRIRIRHRTTCGRPFQQLGPPSERVRLTLVTEIHC
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CDS
(
ORIGIN
Alignment Scores:
Pred. No.: 1,4e-45 Length: 683
Score: 599.00 Matches: 145
Percent Similarity: 73.59% Conservative: 25
Best Local Similarity: 62.77% Mismatches: 41
Query Match: 34.72% Indels: 23
DB: 3 Gaps: 5

US-10-089-278-6 (1-329) x AF240172 (1-683)
QY 92 LeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSer----- 106
Db 668 TTGAAGTGGATGGC-----TGGATAAACNACCCTCTGAAGTCCCAAG 621
QY 107 TyrAsnGlnArg-PheIysGlyIysAlaThrMetThrValAspLysSer---SerAsnTh 125
Db 620 TATGCCAAGAGAGTTCAAGGGACGCTTTGCTCTCTTTGGAAACCTCTGCAGGCAC 561
QY 125 r-AlaTyrIleGluLeuAlaArgLeu-ThrSerGluAspSerAlaIleTyrTyrCysAla 144
```


Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0&t2=MR0-CI0023-241000-102-f09&t3=2000-10-24&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 501.
Location/Qualifiers
1..565
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/dev_stage="Adult"
/clone_lib="CI0023"
/note="Organ: colon; ins; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 2,26e-38 Length: 565
Score: 520.50 Matches: 105
Percent Similarity: 76.36% Conservative: 21
Best Local Similarity: 63.64% Mismatches: 31
Query Match: 30.17% Indels: 8
DB: 2 Gaps: 2

US-10-089-278-6 (1-329) x BF801321 (1-565)

QY 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg 60
DB 35 GCAGCCAGCCGGCCATGTCAGTGAAGTCTGCAGGAGTAAAGCACTGAAGTGAAG 94
QY 61 ProGlyValSerValLysLeuSerCysLys-GlySerGlyTyrThrPheThrAspTyrGl 80
DB 95 CCTGGGGCTTCAGTGAAGTGTCTCTGCAAGTGTCTTGGCTACATCTTCAAGTTATGA 154
QY 80 YMetSerTyrValLysGlnSerHisAlaLysSerLeuGluTyrTrpIleGlyLeuLeuSerTh 100
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QY 140 eTyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrAla-----LeuAspTy 158
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QY 198 rLeuGlyGlnArg 202
DB 500 TCCAGTGGAGAGG 512

RESULT 15
BG965088
LOCUS

738 bp mRNA linear EST 12-JUN-2001

DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

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ORIGIN

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Score: 511.50 Matches: 107
Percent Similarity: 73.49% Conservative: 15
Best Local Similarity: 64.46% Mismatches: 25
Query Match: 29.65% Indels: 19
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US-10-089-278-6 (1-329) x BG965088 (1-738)

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DB 70 GTAGCA-----ACAGCTACAGGT 87
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QY 65 ValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpVal 84
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QY 85 LysGlnSerHisAlaLysSerLeuGluTyrIleGlyLeuIleSerThrTyrTyrGlyAsp 104
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QY 105 ProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsn 124
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mRNA sequence.
BG965088
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EST.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10989 row: 9 column: 15
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Job time : 3123 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 23, 2005, 14:02:29 ; Search time 198 Seconds
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2718.864 Million cell updates/sec

Title: US-10-089-278-6

Perfect score: 1725

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	935.5	54.2	717	4	US-09-473-653-5
5	935	54.2	996	4	US-08-894-922A-4
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13	880	51.0	807	4	US-09-674-677-4	Sequence 4, Appli
14	878	50.9	864	3	US-09-423-439-47	Sequence 47, Appl
15	853.5	49.5	780	4	US-09-526-738A-3	Sequence 3, Appli
16	844.5	49.0	771	4	US-09-526-738A-1	Sequence 1, Appli
17	842	48.8	732	2	US-08-553-497A-19	Sequence 19, Appl
18	837.5	48.6	717	2	US-08-553-497A-17	Sequence 17, Appl
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21	833.5	48.3	1679	2	US-08-661-052-15	Sequence 15, Appl
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ALIGNMENTS

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; Sequence 1, Application US/09070408
; Patent No. 6180341
; GENERAL INFORMATION:
; APPLICANT: Iverson, Brent L.
; APPLICANT: Georgiou, George
; APPLICANT: Burks, Elizabeth A.
; TITLE OF INVENTION: IN VITRO SCANNING SATURATION MUTAGENESIS
; TITLE OF INVENTION: OF PROTEINS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,408
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/045,409
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: McMillian, Nabeela R.
; REGISTRATION NUMBER: P-43,363
; REFERENCE/DOCKET NUMBER: UT5B:593
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000

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; TELEFAX: 512/447-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1010 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-070-408-1

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RESULT 2
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; Sequence 6, Application US/08447402
; Patent No. 5866344
; GENERAL INFORMATION:
; APPLICANT: Iverson, Brent
; APPLICANT: Georgiou, George
; APPLICANT: Chen, Gang
; TITLE OF INVENTION: IMMUNOASSAY AND ANTIBODY SELECTION
; TITLE OF INVENTION: METHODS USING CELL SURFACE EXPRESSED
; TITLE OF INVENTION: LIBRARIES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,402
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/258,543
; FILING DATE: 10-JUN-1994
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/794,731
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSB:584\KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 780 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..780
US-08-447-402-6

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Score: 978.00 Matches: 187
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Best Local Similarity: 74.21% Mismatches: 31
Query Match: 56.70% Indels: 4
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US-10-089-278-6 (1-329) x US-08-447-402-6 (1-780)
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Db 61 TCCTGCAAAATCCTCAGGGTACATTTTCCCGACTTCTACATGAATGGTTCGCCAGTCT 120
Qy 88 HisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107
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RESULT 3

US-08-994-922A-9
; Sequence 9, Application US/08894922A
; Patent No. 5863765
; GENERAL INFORMATION:
; APPLICANT: BERRY, Mark John
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOOT, Cornelius P.E.
; APPLICANT: WHITELAM, Garry Clark
; TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,922A
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9504344.4
; FILING DATE: 03-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00468

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Qy 299 AlaSerGlySerGlyGlyGlyGlySerGlyGlyGly 310
Db 814 -----GGATCCGGTAGCGGGAACCTCCGGTAAGGGG 843
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; Sequence 5, Application US/09473653
; Patent No. 6703015
; GENERAL INFORMATION:
; APPLICANT: Solomon, Beka
; APPLICANT: Frenkel, Dan
; TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY
; FILE REFERENCE: 00/20785
; CURRENT APPLICATION NUMBER: US/09/473,653
; CURRENT FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 60/152,417
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(7)
; OTHER INFORMATION: scFv 508F construct
US-09-473-653-5
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Qy 68 SerCysValysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpValIleGlnSer 87
Db 61 TCCTGCAGAGGTTCTGGCTACACATTCACCTGATGATGCTATGACCTGGGTGAAGCAGAT 120
Qy 88 HialalysSerLeuGluTrpIleGlyLeuIleSerThrTyrGlyAspProSerTyr 107
Db 121 CATGCAAGAGTCTAGAGTGGATTGGAGTTGATGATTAGTACTTACTATGCTGATGCTAGCTAC 180
Qy 108 AsnGlnArgPheIleGlyIleAlaThrMetThrValAspIleSerSerAsnThrAlaTyr 127
Db 181 AACCAGAAAGTTCAGGCAAGGCCAACATGACTGTAGACAAATCCTCCAGCACAGCCAT 240
Qy 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTrpCysAlaArgSerAsp 147
Db 241 ATGGAACCTGCCAGACTGACATCTGAGGATCTGCCATCTATTACTGTGCAAGAGG--- 297
Qy 148 GlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrValThrVal 167
Db 298 GCTACTATGCTCTACTTT-----GACTACTGGGGCCAAAGTACACGGTCCACCGTC 348
Qy 168 SerSerGlyGlyGlySerGlyGlyGlySerGlyGlySerGlyGlySerAspIleGlu 187
Db 349 TCCTCAGGTGAGGCGGTTTCAGGCGGAGTTGGCTCTGGCGGTGGCGGATCGGATCGAG 408

Qy 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
Db 409 CTCACCTAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCCACCATGACCTGC 468
Qy 208 ArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTrpTyrGlnGlnIle 227
Db 469 AGTGCCAGCTCAAGTATA-----AGTTACATGCATCTGGTATCAGCAGAAG 513
Qy 228 ProGlyGlnProProIleLeuLeuIleTyrArgAlaSerAsnLeuGluSerGlyValPro 247
Db 514 CCAGGCACCTCCCCCAAGATGGATTATGACACATCCAAACTGGCTCTCGGATCCCT 573
Qy 248 AlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspProValGlu 267
Db 574 GCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTATTCTCTCACAATCAGCAGCATGGAG 633
Qy 268 GluAspAlaAlaValTyrCysLeuGlnSerMetGluAspProTyrThrPheGly 287
Db 634 GCTGAAGATGCTGCCACTTATTACTGCCATCAGCGGAGTAGTTACCATTCAGGTTCCGA 693
Qy 288 GlyGlyThrLysLeuGluIleLys 295
Db 694 GGGGGGCCAAGCTGGAATATAA 717
RESULT 5
US-08-894-922A-4
; Sequence 4, Application US/08894922A
; Patent No. 5863765
; GENERAL INFORMATION:
; APPLICANT: BERRY, Mark John
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOGT, Cornelius P.E.
; APPLICANT: WHITELAM, Gary Clark
; TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,922A
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9504344.4
; FILING DATE: 03-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00468
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul K.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 60113/341261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)-861-3503
; TELEFAX: (202)-822-0944
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 996 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
US-08-894-922A-4

FRAGME

Db 670 TATGGCAATAGTTTTATGTCAGTGGTACCAGCAGAAACAGGACAGCCAACTCCTC 729
QY 236 IleTyrArgAlaSerAnLeuGluSerGlyValProAlaArgPheSerGlySerGlySer 255
Db 730 ATCTATCGTCATCCCAACCTAGAACTGGGATTCCTGCCAGGTTCTAGTGGCACTGGGTCT 789
QY 256 GluSerAspPheThrLeuThrIleAspProValGluGluAspAlaAlaValTyrTyr 275
Db 790 AGACAGAGACTTCACCTCCACCAATAATCTGTGGAGGCTGATGTTGCAACCTATTAT 849
QY 276 CysLeuGlnSerMetGluAspPro-----TyrThrPheGlyGlyThrLysLeuGlu 293
Db 850 TGTCAACAAAGTATGATGATTCCTCGTACATGTCACGCTTCGGAGGGGGACCAAGCTCGAG 909
QY 294 IleLysArgAlaAlaAlaSerGlySerGlyGlyGlyGlySerGlyGlyGly 310
Db 910 ATCAACCG-----GGATCCGGTAGCGGGAACCTCCGGTAAGGGG 948
RESULT 7
US-09-486-814A-1
; Sequence 1, Application US/09486814A
; Patent No. 6562599
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Masato
; APPLICANT: HAYASHI, No. 656259910
; APPLICANT: YAMAMOTO, Hiroko
; APPLICANT: TOHDOH, Naoki
; TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS B VIRUS CORE
; TITLE OF INVENTION: PROTEIN, GENE THEREOF, AND THERAPEUTIC AGENT FOR
; TITLE OF INVENTION: HEPATITIS B CONTAINING THESE
; FILE REFERENCE: 0020-4682P
; CURRENT APPLICATION NUMBER: US/09/486, 814A
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Mus sp., strain: Balb/c, tissue: spleen
; FEATURE:
; OTHER INFORMATION: Clone: pzeoSV1C9
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(891)
; OTHER INFORMATION: Identification Method: E
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(111)
; OTHER INFORMATION: Encoding PRE-HV sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (436)..(528)
; OTHER INFORMATION: Encoding a linker sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (838)..(891)
; OTHER INFORMATION: Encoding a TAIL sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(894)
; OTHER INFORMATION: strandedness: double-stranded
US-09-486-814A-1
Alignment Scores:
Pred. No.: 2,42e-72 Length: 894
Score: 918.50 Matches: 182
Percent Similarity: 77.09% Conservative: 30
Best Local Similarity: 66.18% Mismatches: 47
Query Match: 53.25% Indels: 17
DB: 4 Gaps: 4
US-10-089-278-6 (1-329) x US-09-486-814A-1 (1-894)

QY 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnInSerGlyAlaGluLeuValArg 60
Db 97 GGGGCCAGCCCGCCATGGCCAGGTGAAGCTGCAGGAGTCAGGACCTGAGCTGGAGAAG 156
QY 61 ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
Db 157 CCTGGCGCTTCAGTGAAGATATCTGCAAGGCTTCTGGTTACTCATTTCACTGGCTACAAC 216
QY 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
Db 217 ATGAAGTGGGTGAAACAGAGCAATGGAAGACCTTGAGTGGATTGGATATATTATTCCT 276
QY 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db 277 TCAATATGGTGTACTGGCTACCAACAGAGTTCAGAGCAAGCCACATTTGCTGTAGAC 336
QY 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db 337 AAATCCTCCAGCACAGCCTACATGCAACTGAGCAGCCTGACATCTGAGGACTCTGCAGTC 396
QY 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGly 160
Db 397 TATTACTGTGCAAGA-----CTGGGACTTGACTACTCGGGC 432
QY 161 GlnGlyThrThrValThrValSerSerGlyGlyGlyGlySerGlyGlyGlySerGly 180
Db 433 CAAGGACCAACGGTACCGCTCTCTCAGTGGAGGGGGTTCAGGCGGAGGTGGCTCTGGC 492
QY 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200
Db 493 GGTGGCGGATCGGACATCGAGCTCACTCAGTCTCCAACCAACCATGGCTGCATCTCCCGG 552
QY 201 GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220
Db 553 GAGAAGATCACTATCACCTGCAGTGCAGCTCAAGTATAAGTTCC-----AAITAC 603
QY 221 MetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSer 240
Db 604 TTGCATTGGTATCAGCAGAGCCAGGATTCCTCCCTAAACTCTTGATTATAGGACATCC 663
QY 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260
Db 664 AATCTGGCTTCTGGAATCCAGCTCGCTTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCT 723
QY 261 LeuThrIleAspProValGluGluAspAlaAlaValTyrTyrCysLeuGlnSerMet 280
Db 724 CTCACAAATTGGCACCACATGGAGGCTGAAGATGTTGCCACTTACTTCCAGCGAGGTAGT 783
QY 281 GluAspPro-----TyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAla 298
Db 784 AGTATACCAACGCATATTCAGTTCGGTGGTGGGACAAAGTTGGAATATAAACCGCGGCC 843
QY 299 AlaSerGlySerGlyGlyGlySerGlyGlySerGlyGlySerGlyGly 313
Db 844 GCA-----GGTGC-GCCGGTCCGTATCCGGATCCGCTGGA 878
RESULT 8
US-08-894-922A-13
; Sequence 13, Application US/08894922A
; Patent No. 5863765
; GENERAL INFORMATION:
; APPLICANT: BERRY, Mark John
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOGT, Cornelius P.E.
; APPLICANT: WHITEHAM, Gary Clark
; TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.

COUNTRY: United States
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,922A
FILING DATE: 03-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9504344.4
FILING DATE: 03-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/00468
FILING DATE: 01-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kokulis, Paul K.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 60113/241261
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)-861-3503
TELEFAX: (202)-822-0944
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA
US-08-894-922A-13

Alignment Scores:
Pred. No.: 3.13e-72 Length: 797
Score: 916.50 Matches: 186
Percent Similarity: 76.87% Conservative: 20
Best Local Similarity: 69.40% Mismatches: 41
Query Match: 53.13% Indels: 21
DB: 2 Gaps: 4

US-10-089-278-6 (1-329) x US-08-894-922A-13 (1-797)

QY 45 AlaMetAlaGluValLysLeuGlnSerGlyAlaGluValArgProGlyValSer 64
DB 3 GCTTACCTACAGGTGCGAGCTGCGAGCTGCGGCTGAAGTGGTGAAGCTGGGCTTCT 62
QY 65 ValLysLeuSerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTyrVal 84
DB 63 GTGAGCTGTCTGCAAGGCTTCGACTACACCTTACAGTATTATGGATGCACTGGTG 122
QY 85 LysGlnSerHisAlaLysSerLeuGluTyrPheGlyLeuLeuSerThrTyrTyrGlyAsp 104
DB 123 AAGCAGAGGCTGCGACAGGCTTGAAGTGGATGGAGAGATTAACTTACCAACGGTCT 182
QY 105 ProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerAsn 124
DB 183 ACTTATTACAAATGAGAAGTTCAAGAGCAAGGCCACACTGCTAGCAAAATCTCCAGT 242
QY 125 ThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAla 144
DB 243 ACAGCTTACATGAGCTACAGAGCTGACATCTGAGGACTCTGGGCTCTATTACTGTGCA 302
QY 145 ArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTyrPheGlnGlyThrThr 164
DB 303 AGACGGTATGGTAAC-----TCCTTTTACTTGGGCGCAAGGACCAACG 347
QY 165 ValThrValSerSerGlyGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlySer 184
DB 348 GTACCGGTCTCC-----TCACGAATGGATAAAGG 377
QY 185 AspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThr 204

378 GACATCGAGCTCACCAGTCTCCAGATTCTTTGGCTGTCTCTAGGGCAGAGGGCCACC 437
205 ILeSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTyrTyr 224
438 ATATCTCTGCAGAGCCAGTGAAGTGTGTATGATGTTATGGCAATAGTTTTATGTCAGTGGTAC 497
225 GlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSer 244
498 CAGCAGAAACAGACAGCCACCACCAAACTCTCTATCTATCTGTCATCAACCTAGAATCT 557
245 GlyValProAlaArgPheSerGlySerGlySerGlySerGlySerPheThrLeuThrIleAsp 264
558 GGGATCTCTGCCAGTTCAGTGGCACTGGTCTAGGACAGACTTCCACCTCACCATTAAAT 617
265 ProValGluGluAspAspAlaAlaValTyrCysLeuGlnSerMetGluAspPro--- 283
618 CTTGTGGAGGCTGATGATGTTGCAACCTATTATTGTCAAAAGTATGATATCCGTAC 677
284 ---TyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAlaSerGlySer 302
678 ATGTACACGTTCCGAGGGGGGCAAGCTCGAGATCAACGG-----GGATCC 725
303 GlyGlyGlyGlySerGlyGly 310
726 GGTAGCGGAACCTCCGTAAGGG 749

RESULT 9
US-09-423-439-31
Sequence 31, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSER: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-NOV-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 2019 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-423-439-31

Alignment Scores:
Pred. No.: 6.01e-71 Length: 2019
Score: 908.00 Matches: 179
Percent Similarity: 76.70% Conservative: 35
Best Local Similarity: 64.16% Mismatches: 45
Query Match: 52.64% Indels: 20
DB: 3 Gaps: 5

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US-10-089-278-6 (1-329) x US-09-423-439-31 (1-2019)
QY 48 GluValLysLeuGlnGlnSerGlyAlaGluLeuValArgProGlyValSerValLysIle 67
Db 58 CAGGTCCTCAACTGCAGCAGCGCTGGGGCTGAACCTGGTGAAGCCTGGGGCTTCAGTGCAGCTG 117
QY 68 SerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpValLysGlnSer 87
Db 118 TCTGCAAGGCTTCTGGCTACACTTCACCGGTACTGGATACCTGGGTGAAGCAGAGG 177
QY 88 HisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107
Db 178 CCTGGACAAGCCTTCAGCTGGATTGGAGAGGTTAATCTAGTACCGGTCGTTCTGACTAC 237
QY 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
Db 238 AATGAGAAGTTCAAGAACCAAGGCCACACTGACTGTAGACAAATCTCCACACAGCCTAC 297
QY 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAsp 147
Db 298 ATGCAACTCAGCAGCCTGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA---GAG 354
QY 148 GlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrThrValThrVal 167
Db 355 AGGGCCATGGTTACACCGATGCTATGAGTACTGGGGCCCAAGGACACCGGTCCACCGTC 414
QY 168 SerSerGlyGlyGlyGlySerGlyGlyGlySerGlyGlySerGlyGlySerAspIleGlu 187
Db 415 TCCTCAGGTGGCGGTGGCTCGGGCTGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG 474
QY 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
Db 475 CTCTCAGAGTCTCCATCTCCCTGGCTGTGTACAGCAGAGAGAGAGGTCCACCATGAGCTGC 534
QY 208 ArgAlaSerGluSerVal-----AspSerTyrGlyAspSerPheMetHisTrpTyrGln 225
Db 535 AATCCAGTCAGAGTCTCTCTCAACAGTACAGAACCCGAAAGACTACTTGGCTTGGTACCAG 594
QY 226 GlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGly 245
US-10-089-278-6 (1-329) x US-09-423-439-37 (1-2025)
QY 48 GluValLysLeuGlnGlnSerGlyAlaGluLeuValArgProGlyValSerValLysIle 67
Db 58 CAGGTCCTCAACTGCAGCAGCGCTGGGGCTGAACCTGGTGAAGCCTGGGGCTTCAGTGCAGCTG 117
QY 68 SerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpValLysGlnSer 87
Db 118 TCTGCAAGGCTTCTGGCTACACTTCACCGGTACTGGATACACTGGGTGAAGCAGAGG 177
QY 88 HisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107
Db 178 CCTGGACAAGCCTTCAGCTGGATTGGAGAGGTTAATCTAGTACCGGTCGTTCTGACTAC 237
QY 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
Db 238 AATGAGAAGTTCAAGAACCAAGGCCACACTGACTGTAGACAAATCTCCACACAGCCTAC 297
QY 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAsp 147
Db 298 ATGCAACTCAGCAGCCTGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA---GAG 354
QY 148 GlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrThrValThrVal 167
Db 355 AGGGCCATGGTTACACCGATGCTATGAGTACTGGGGCCCAAGGACACCGGTCCACCGTC 414
QY 168 SerSerGlyGlyGlyGlySerGlyGlyGlySerGlyGlySerGlyGlySerAspIleGlu 187
Db 415 TCCTCAGGTGGCGGTGGCTCGGGCTGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG 474
QY 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
Db 475 CTCTCAGAGTCTCCATCTCCCTGGCTGTGTACAGCAGAGAGAGGTCCACCATGAGCTGC 534
QY 208 ArgAlaSerGluSerVal-----AspSerTyrGlyAspSerPheMetHisTrpTyrGln 225
Db 535 AATCCAGTCAGAGTCTCTCTCAACAGTACAGAACCCGAAAGACTACTTGGCTTGGTACCAG 594
QY 226 GlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGly 245
Alignment Scores:
Pred. No.: 6 03e-71 Length: 2025
Score: 908.00 Matches: 179
Percent Similarity: 76.70% Conservative: 35
Best Local Similarity: 64.16% Mismatches: 45
Query Match: 52.64% Indels: 20
DB: 3 Gaps: 5
US-10-089-278-6 (1-329) x US-09-423-439-37 (1-2025)
QY 48 GluValLysLeuGlnGlnSerGlyAlaGluLeuValArgProGlyValSerValLysIle 67
Db 58 CAGGTCCTCAACTGCAGCAGCGCTGGGGCTGAACCTGGTGAAGCCTGGGGCTTCAGTGCAGCTG 117
QY 68 SerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpValLysGlnSer 87
Db 118 TCTGCAAGGCTTCTGGCTACACTTCACCGGTACTGGATACACTGGGTGAAGCAGAGG 177
QY 88 HisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107
Db 178 CCTGGACAAGCCTTCAGCTGGATTGGAGAGGTTAATCTAGTACCGGTCGTTCTGACTAC 237
QY 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
Db 238 AATGAGAAGTTCAAGAACCAAGGCCACACTGACTGTAGACAAATCTCCACACAGCCTAC 297
QY 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAsp 147
Db 298 ATGCAACTCAGCAGCCTGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA---GAG 354
QY 148 GlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrThrValThrVal 167
Db 355 AGGGCCATGGTTACACCGATGCTATGAGTACTGGGGCCCAAGGACACCGGTCCACCGTC 414
QY 168 SerSerGlyGlyGlyGlySerGlyGlyGlySerGlyGlySerGlyGlySerAspIleGlu 187
Db 415 TCCTCAGGTGGCGGTGGCTCGGGCTGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG 474
QY 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
Db 475 CTCTCAGAGTCTCCATCTCCCTGGCTGTGTACAGCAGAGAGAGGTCCACCATGAGCTGC 534
QY 208 ArgAlaSerGluSerVal-----AspSerTyrGlyAspSerPheMetHisTrpTyrGln 225
Db 535 AATCCAGTCAGAGTCTCTCTCAACAGTACAGAACCCGAAAGACTACTTGGCTTGGTACCAG 594
QY 226 GlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGly 245
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 2025 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-423-439-37
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RESULT 10

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US-09-423-439-37
Sequence 37, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
```

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Db 595 CAGAGACAGGGCAGTCTCTAAACTGCTGATCTATTGGGCATCCACTAGACATCTGGG 654
Qy 246 ValProAlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspPro 265
Db 655 GTCCCTGATCGCTTCACAGGCGAGTGGATCTCTGGGACAGATTTCACTCTCACCATCAGCAGT 714
Qy 266 ValGluGluAspAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyr--- 284
Db 715 GTGAGCGCTGAGACCTGGCAATTTATTACTGCAAGCAATCT-----TAACT 762
Qy 285 -----ThrPheGlyGlyThrLysLeuGluLeuLysArgAlaAlaAspGlySer 302
Db 763 CTTCGGACGTTCCGTGAGGCGACCAAGCTCGAGATCAACGG----- 804
Qy 303 GlyGlyGlyGlySerGlyGlyGlySerGlySerGlyGlyGlyGlyGlyGlyGlySer 321
Db 805 -----GGCGGTGGTGGTCCGCGAGGTGGCGGTAGCGGTGGCGGGGTTC 849

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RESULT 11

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; US-08-403-853-17
; Sequence 17, Application US/08403853
; Patent No. 5844094
; GENERAL INFORMATION:
; APPLICANT: HUDSON, Peter J.
; APPLICANT: LAH, Maria
; APPLICANT: KORRT, Alex A.
; APPLICANT: IRVING, Robert A.
; APPLICANT: ATWELL, John L.
; APPLICANT: MALEY, Robyn L.
; APPLICANT: POWER, Barbara E.
; APPLICANT: COLMAN, Peter M.
; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,853
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/AU93/00491
; FILING DATE: 24-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL 4973
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16786/189/CHAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 1..819

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..819
; US-08-403-853-17
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Pred. No.: 2,93e-70 Length: 831
Score: 894.50 Matches: 171
Percent Similarity: 79.61% Conservative: 32
Best Local Similarity: 67.06% Mismatches: 47
Query Match: 51.86% Indels: 5
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Qy 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg 60
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Qy 61 ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
Db 106 CTTGGGGCCCTCAGTGAGGATGCTCTCAAGGCTTCTGGCTACACATTTTACCAATTA 165
Qy 81 MetSerTyrValLysGlnSerHisAlaLysSerLeuGluTyrIleGlyLeuIleSerThr 100
Db 166 ATGTACTGGGTAAACACAGTCACCTGCAGCGGCTGGAGTGGATTTGGAAATTTTATCCA 225
Qy 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db 226 GGAATGGTGATACTTCTTACATCAGAGTTTCAAGACAAAGCCACATTCATGCTGCTG 285
Qy 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db 286 AAATCTCTCAACACAGCTACATGCAGCTCAGCAGCTGCAGAGCTGCACATCTGCGGTC 345
Qy 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrAlaLeuAspTyrTyrGly 160
Db 346 TATTACTGTGCAAGATCGGGGGCTCTATAGATACAGCGAGCTTTGACTCTGGGGC 405
Qy 161 GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlyGlySerGly 180
Db 406 CAAGGACCCACCGGTCCCGTC---TCCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 462
Qy 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200
Db 463 GGTGGTGGTTCGGATATCGAGCTCACACAGACTACATCTCCCTCTGCTGCTCTCTG 522
Qy 201 GlnArgAlaThrIleSerCysArgAlaSerValAspSerValAspSerTyrGlyAspSerPhe 220
Db 523 GACAGAGTCACCATCAGTTGCAGGGCAAGTCAGGACATTAAGTAATAT----- 570
Qy 221 MetHisTyrTyrGlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArgAlaSer 240
Db 571 TTAAACTGGTATCAACAGAAATCCAGATGGAACCTGTTAACTCCTGATCTACTACATCA 630
Qy 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260
Db 631 AATTTACACTCAGAAAGTCCCATCAGCGTTTCAGTGGCAGTGGGTCTGGAACAGATATTCT 690
Qy 261 LeuThrIleAspProValGluAspAspAlaAlaValTyrTyrCysLeuGlnSerMet 280
Db 691 CTCACCATTAGCAACCTGGAAACAAAGATATTGCCACTTACTTTTGGCCAAAGGATTTT 750
Qy 281 GluAspProTyrThrPheGlyGlyThrLysLeuGluLeuIleLys 295
Db 751 ACGTTTCGGTTCAGGTTCCGAGGGGGGACCAAGCTCGAGATAAGA 795

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RESULT 12

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; US-09-203-958A-3
; Sequence 3, Application US/09203958A
; Patent No. 6682928
; GENERAL INFORMATION:
; APPLICANT: KELER, Tibor

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Qy 86 GlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspPro 105
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Qy 106 SerTyrAenGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThr 125
Db 183 AACTACCAACCAAGAGTTTGGAGCCCAAGCCCAATGACTGTAGACAAATCCTCCCAACACA 242
Qy 126 AlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArg 145
Db 243 GGCTATTGGAACTTGCAGATTCGACATCTGAGGATTCCTGCCATCTATTACTGTGCAAGA 302
Qy 146 SerAspGlyAenTyrGlyTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrVal 165
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Qy 166 ThrValSerSerGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlyGlySerAsp 185
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Qy 186 IleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIle 205
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Qy 206 SerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTyrTyrGln 225
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Qy 226 GlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGly 245
Db 513 CAGAAGTCAGGCACCTCCCCCAAAAGATGGATTATGACACATCCAACTGGCTCTGGA 572
Qy 246 ValProAlaArgPheSerGlySerGlySerGlySerGluSerAspPheThrIleAspPro 265
Db 573 GTCCCTCTCGCTTCACTGGCAGTGGGTCTGGGACCTCTCACTCTCTCACAATCAGCAGC 632
Qy 266 ValGluGluAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThr 285
Db 633 TTGAGGCTGAAGATGCTGCCACTTATTACTGCGACACTGGGAGTAGTAACCTCCACG 692
Qy 286 PheGlyGlyThrLysLeuGluIleLysArgAlaAla 299
Db 693 TTCGGTCTGGGACCAAGCTGGAAATAAACGGGCGGCCGA 734

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; Sequence 47, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillebury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09423.439
; FILING DATE: 09-No. 6339070-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
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; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-423-439-47
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Pred. No.: 8,87e-69 Length: 864
Score: 878.00 Matches: 172
Percent Similarity: 79.31% Conservative: 35
Best Local Similarity: 65.90% Mismatches: 44
Query Match: 50.90% Indels: 10
DB: 3 Gaps: 4
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Qy 61 ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
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Qy 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
Db 166 ATACACTGGGTGAAGCAGGAGCCCTGAGCAAGGCTTGGAGTGGATGGAGAGTTAATCCT 225
Qy 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db 226 AGTACCGGTCTGCTGACTACATGAGAGTTCACAGAACAGGCCACACTGACTGTAGAC 285
Qy 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db 286 AATCTCTCCACCACAGCCTACATGCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTC 345
Qy 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGly 160
Db 346 TATTACTGTGCAAGA--GAGAGGGCTATGTTACAGCATGCTATGGACTACTGGGGC 402
Qy 161 GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlyGlySerGly 180
Db 403 CAAGGGACCAACGGTCAACCGTCTCTCAGGTGGCGGTGGCTCGGGCGGTGGTGGGT 462
Qy 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerSerLeuAlaValSerLeuGly 200
Db 463 GCGCGCGGATCTGACATTGAGCTCTCACAGTCTCCATCTCTCCCTGCTGTGTGAGCAGGA 522
Qy 201 GlnArgAlaThrIleSerCysArgAlaSerGluSerVal-----AspSerTyrGlyAsp 218
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Qy 219 SerPheMetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArg 238
Db 583 AACTACTTGGCTTGGTACCAGCAGACAGCAGGCGGAGTCTCTCTAACTGCTGATCTATTGG 642
Qy 239 AlaSerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAsp 258
Db 643 GCATCCACTAGGACATCTGGGGTCCCTGATCGCTTTCACAGGCACTGGATCTGGGACAGAT 702
Qy 259 PheThrLeuThrIleAspProValGluGluAspAlaValTyrTyrCysLeuGln 278
Db 703 TTCACCTCTCACCATCAGCAGTGTGAGGCGGTGAAGACCTGCAATTTATTACTCAAGCAA 762
Qy 279 SerMetGluAspProTyr-----ThrPheGlyGlyGlyThrLysLeuGluIleLys 295
Db 763 TCT-----TATACTCTTCGGACGCTTCGGTGGAGGACCAAGCTCGAGATCAA 810
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QY 296 Arg 296
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RESULT 15

US-09-526-738A-3

; Sequence 3, Application US/09526738A

; Patent No. 6630584

; GENERAL INFORMATION:

; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT

; APPLICANT: LTD.

; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53

; FILE REFERENCE: 1196336

; CURRENT APPLICATION NUMBER: US/09/526, 738A

; CURRENT FILING DATE: 2000-03-16

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 780

; TYPE: DNA

; ORGANISM: Humanus

US-09-526-738A-3

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DB:	4	Gaps:	4

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QY	66	LyAlaSerCysLysGlySerGlyThrPheThrAspTyrGlyMetSerTrpValLys	85
Db	61	AAGATGTCCTGCAAGACTTCTGGCTACACCTTTACTAGCTACTGGATGAACCTGGTAAAA	120
QY	86	GlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspPro	105
Db	121	CAGAGGCTCGACAGGCTCTGGAATGGATTGGATACATTAACTACCACCTGGTTACT	180
QY	106	SerTyrAsnGlnArgPheLysGlyAlaThrMetThrValAspLysSerSerAsnThr	125
Db	181	AAGTACAATCAGAAGTTCAAGGACCAAGCCACATTGACTGCACACAAATCCTCCAGCAG	240
QY	126	AlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArg	145
Db	241	GCCTACATGCAACTGACGACCTGACCACTGAGCTCTGCAGTCTATTATTATTGACAACT	300
QY	146	SerAspGlyAsnTyrGlyTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrVal	165
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QY	166	ThrValSerSerGlyGlyGlySerGlyGlySerGlyGlyGlyGlyGlySerAsp	185
Db	343	ACCGTCTCCTCAGGTGGAGGCGGTTCAGGGCGAGGTGGCTCTGGCGGTGGCGGATCGGAC	402
QY	186	IleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGlnArgAlaThrIle	205
Db	403	ATCAGCTCACTAGTCTCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCAACATA	462
QY	206	SerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTrpTyrGln	225
Db	463	ACCTGCAGTGCACGCTCAAGTGA-----AATTACATGCACCTGGTTCAG	507
QY	226	GlnLysProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGly	245
Db	508	CAGAAAGCCAGCACTTCTCCCAAACTCTGGATTCTTAGCACATCCAAACCTGGCTTCTGGA	567

QY	246	ValProAlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspPro	265
Db	568	GTCCCTGCTCGCTTCAGTGGCAGTGGATCTGGGACCTCTTACTCTCTCACAATCAGCCGG	627
QY	266	ValGluGluAspAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThr	285
Db	628	ATGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAAGGAGTAGTTACCCATACACG	687
QY	286	PheGlyGlyThrLysLeuGluIleLysArgAlaAlaSerGlySerGlyGlyGly	305
Db	688	TTCCGAGGGGGCCACCAAGCTGCAAAATCAAAACGGGGCGCCGCA-----GGTGC-GCC	737
QY	306	GlySerGlyGlySerGlyGly 313	
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Search completed: August 23, 2005, 16:43:48

Job time : 206 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 23, 2005, 14:42:34 ; Search time 8176 Seconds
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Title: US-10-089-278-6

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS-human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODES=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	978	56.7	780	11	US-09-813-444-1 Sequence 1, Appli
4	976.5	56.6	1817	21	US-10-489-626-4 Sequence 4, Appli
5	948.5	55.0	1906	21	US-10-491-653-25 Sequence 25, Appli
6	947.5	54.9	756	16	US-10-169-351-68 Sequence 68, Appli
7	935.5	54.2	717	9	US-09-808-037-5 Sequence 5, Appli
8	935.5	54.2	717	14	US-10-162-889-5 Sequence 5, Appli
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19	917.5	53.2	1605	18	US-10-257-864A-32 Sequence 32, Appli
20	917.5	53.2	1605	18	US-10-221-131-32 Sequence 32, Appli
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36	883	51.2	828	20	US-10-645-085A-24 Sequence 24, Appli
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42	878	50.9	828	18	US-10-221-131-24 Sequence 24, Appli
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ALIGNMENTS

RESULT 1

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; Sequence 1, Application US/09782672
; Publication No. US20030036092A1
; GENERAL INFORMATION:

APPLICANT: Iverson, Brent
Georgiou, George
Chen, Gang
Olsen, Mark J.

Daugherty, Patrick S.
TITLE OF INVENTION: Directed Evolution of Enzymes and
Antibodies

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARNOLD, WHITE AND DURKEE

STREET: P.O. Box 4433


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QY 88 HisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrglyAspProSerTyr 107
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QY 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
DB 181 AACCCAGAGTTTAAAGTAAGGCACCCCTTACTGTGCACAAATCTTCTCAACTGCTTAC 240
QY 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrglyAspProSerAsp 147
DB 241 ATGAGCTGGCTTCTTGACCTCTGAGGACTCGCGGTATCTATTTGGGGTCTAGCGTCTCTCT 300
QY 148 GlyAsnTyrGlyTyrTyrglyAlaLeuAspTyrTrpGlyGlnGlyThrValThrVal 167
DB 301 GGTAAC-----AAATGGGCCATGATTTATGGGGTCATGGTGTCTAGCGTCTCTCTG 351
QY 168 SerSerGlyGlyGlySerGlyGlyGlySerGlyGlySerGlyGlySerAspIleGlu 187
DB 352 AGCTCTGGTGGCGGTGGCTCGGGCGGTGGTGGGTGGCGGTGGCGGATCAGACATAGTA 411
QY 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
DB 412 CTGACCCAGTCTCAGCTTCTTGGCTGTCTCTAGGACAAAGGGCCACGATATCTCTGC 471
QY 208 ArgAlaSerGluSer---ValAspSerTyrGlyAspSerPheMetHisTrpTyrGlnGln 226
DB 472 CGATCCAGCCAAAGTCTCGTACATTTCTAATGGTAATACTTATCTGAATCTGGTACCAACAG 531
QY 227 LysProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGlyVal 246
DB 532 AAACCCAGGACAGCCACCAAGCTTCTCATCTATAAGGTATCCAACCGATTTCTCTGGAGTC 591
QY 247 ProAlaArgPheSerGlySerGlySerGlySerGluSerAspPheThrLeuThrIleAspProVal 266
DB 592 CCTGCCAGGTCAGTGGCAGTGGGTCTGAGTCAGACTTCACCTCACCATCGATCCTCTGTG 651
QY 267 GluGluAspAlaAlaValTyrTyrglyLeuGlnSerMetGluAspProTyrThrPhe 286
DB 652 GAGGAGATGATGCTGCATATATTAATCTGTAGGCNAACTAGGCATGTTCCACCCAGTTC 711
QY 287 GlyGlyGlyThrLysLeuGluIleLysArgAlaAla 298
DB 712 GGCTCGGGGACCAAGCTGGAGCTGAAACGTGCTAGC 747
```

RESULT 3

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US-09-813-444-1
; Sequence 1, Application US/09813444
; Publication No. US20040072740A1
; GENERAL INFORMATION:
; APPLICANT: Iverson, Brent
;              Georgiou, George
;              Chen, Gang
;              Olsen, Mark J.
;              Daugherty, Patrick S.
; TITLE OF INVENTION: Directed Evolution of Enzymes and
;                   Antibodies
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE AND DURKEE
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,444
; FILING DATE: 20-Mar-2001
; CLASSIFICATION: <Unknown>
```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/847,063
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSB620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 780 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..780
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-813-444-1
Alignment Scores:
Pred. No.:      8.6e-82      Length:      780
Score:          978.00      Matches:     187
Percent Similarity: 86.11%   Conservative: 30
Best Local Similarity: 74.21% Mismatches:     31
Query Match:     56.70%     Indels:       4
DB:              11         Gaps:        2
US-10-089-278-6 (1-329) x US-09-813-444-1 (1-780)
```

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QY 48 GluValLysLeuGlnGlnSerGlyAlaGluLeuValArgProGlyValSerValLysIle 67
DB 1 GAAGTTCAACTGCAACAGCTGGTCTCTGAATTTAAACCTTGCSCCTCTGTGGCGCATG 60
QY 68 SerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpValLysGlnSer 87
DB 61 TCTGCAAAATCCTCAGGGTACATTTTACCGACTTCTACATGAATTTGGTTCCCGAGTCT 120
QY 88 HisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrglyAspProSerTyr 107
DB 121 CATGGTAAGTCTCTAGACTACATCGGGTACATTTTCCCATACTCTCGGGTTACCGGCTAC 180
QY 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
DB 181 AACCCAGAGTTTAAAGTAAGGCACCCCTTACTGTGCACAAATCTTCTCAACTGCTTAC 240
QY 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrglyAspProSerAsp 147
DB 241 ATGAGCTCGGTCTTGTGACCTCTGAGGACTCGCGGTATCTATTTGGCGCGGCTCTCTCT 300
QY 148 GlyAsnTyrGlyTyrTyrglyAlaLeuAspTyrTrpGlyGlnGlyThrValThrVal 167
DB 301 GGTAAC-----AAATGGGCCATGATTTATGGGGTCTAGCGTCTAGCGTCTCTCTG 351
QY 168 SerSerGlyGlyGlySerGlyGlyGlySerGlyGlySerGlyGlySerAspIleGlu 187
DB 352 AGCTCTGGTGGCGGTGGCTCGGGCGGTGGTGGGTGGCGGCGGATCAGACATAGTA 411
QY 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
DB 412 CTGACCCAGTCTCCAGCTTCTTGGCTGTGTCTCTAGGACAAAGGGCCACGATATCTCTGC 471
QY 208 ArgAlaSerGluSer---ValAspSerTyrGlyAspSerPheMetHisTrpTyrGlnGln 226
DB 472 CGATCCAGCCAAAGTCTCGTACATTTCTAATGGTAATACTTATCTGAATCTGGTACCAACAG 531
QY 227 LysProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGlyVal 246
DB 532 AAACCCAGGACAGCCACCAAGCTTCTCATCTATAAGGTATCCAACCGATTTCTCTGGAGTC 591
QY 247 ProAlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspProVal 266
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Db 592 CCTGCCAGGTTCAAGTGGCAGTGGGTTCTAGTCAGACTTACCCCTCACCATCGATCCTGTG 651
Qy 267 GluGluAspAlaValTyrCysLeuGlnSerMetGluAspProTyrThrPhe 286
Db 652 GAGGAAGATGATGCTGCAATATATTACTGTAGCAAAACATACGATGTTCCACCACGTTTC 711
Qy 287 GlyGlyGlyThrLysLeuGluLeuLysArgAlaAla 298
Db 712 GGCTCGGGACCAAGCTGGAGCTGAAACGTGCTAGC 747

RESULT 4
US-10-489-626-4
; Sequence 4, Application US/10489626
; Publication No. US20050079170A1
; GENERAL INFORMATION:
; APPLICANT: LEGALL, Fabrice
; APPLICANT: KIPRIYANOV, Sergey
; APPLICANT: REUSCH, Uwe
; APPLICANT: MOLDENHAUER, Gerhard
; APPLICANT: LITTLE, Melvyn
; TITLE OF INVENTION: DIMERIC AND MULTIMERIC ANTIGEN BINDING STRUCTURE
; FILE REFERENCE: 03528.0142.PCUS00
; CURRENT APPLICATION NUMBER: US/10/489, 626
; CURRENT FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 1817
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Plasmid
US-10-489-626-4

Alignment Scores:
Pred. No.: 3,08e-81 Length: 1817
Score: 976.50 Matches: 195
Percent Similarity: 79.37% Conservative: 32
Best Local Similarity: 68.18% Mismatches: 54
Query Match: 56.61% Indels: 5
DB: 21 Gaps: 3

US-10-089-278-6 (1-329) x US-10-489-626-4 (1-1817)
Qy 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg 60
Db 168 GCAGCTCAGCCGGCCATGGCGCAGGTGCAACTGCAGCGTCTGGGGCTGAGCTGGTAGG 227
Qy 61 ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
Db 228 CCTGGGTCCTCAGTGAAGATTCTCTGCAAGGCTTCGGCTATGCAATTCAGTAGCTACTGG 287
Qy 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
Db 288 ATGAACCTGGGTGAAGCAGAGCGCTCGCAGAGGCTTCAGTGGATTGGACAGATTGGCCCT 347
Qy 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db 348 GGAGATGGTGATCACTAATGAAAGTTGAAAGTTCAAGGGTAAAGCCACTCTGACTGCAGAC 407
Qy 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db 408 GAATCCTCCAGCAGAGCTACATGCAACTCAGCAGCTAGCACTGAGGACTCTGCGGTC 467
Qy 141 TyrTyrCysAlaArgSerAspGlyAsnTyr-----GlyTyrTyrTyrAlaLeuAspTyr 158
Db 468 TATTTCTGTGTGACAGACGGGAGCTACGACGGTAGGCGGTATTACTACTATGCTATGGAATAC 527
Qy 159 TrpGlyGlnGlyThrThrValThrValSerSerGlyGlyGlyGlySer-----GlyGly 176
Db 528 TGGGGTCAAGGAACCTCAGTCACCGCTCTCTCTCCGCCAAAACAACACCACCAAGCTTGAAGAA 587
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Qy 177 GlyGlySerGlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAla 196
Db 588 GGTGAATTTTCAGAACGACGCGTAGATATCTTGTCTCACCCAAACTCCAGCTCTTTGGCT 647
Qy 197 ValSerLeuGlyGlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyr 216
Db 648 GTGTCTCTAGGCGAGAGGCCACCATCTCTCCAAAGGCCAGCCAAAGTGTGATTATGAT 707
Qy 217 GlyAspSerPheMetHisTrpTyrGlnGlnLysProGlyGlnProProLysLeuLeuIle 236
Db 708 GGTGATAGTTATTGAACTGGTACCAACAGATTCACGAGCAGCCACCAACTCTCTCATC 767
Qy 237 TyrArgAlaSerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGlu 256
Db 768 TATCATGCATCCAATCTAGTTTCTGGATCCACCCAGGCTTTAGTGGCAGTGGGTCTGGG 827
Qy 257 SerAspPheThrLeuThrIleAspProValGluGluAspAlaValTyrTyrCys 276
Db 828 ACAGACTTCACCTCAACATCCATCTCTGGAGAGAGGTGGTGCCTGCAACCTTATCACTGT 887
Qy 277 LeuGlnSerMetGluAspProTyrThrPheGlyGlyGlyThrLysLeuGluLeuLysArg 296
Db 888 CAGCAAGTACTGAGGATCCGTGGAGCTTCGGTGGAGGCCACCAAGCTGGAAATCAACCG 947
Qy 297 AlaAlaAlaSerGlySerGlyGlyGlySer---GlyGlyGlySerGlyGlyGlyGly 315
Db 948 GCTGATGCTGCGGCCGCTGGTGGTGGTCTTCTGGCGCGCGTGGTAGCGGTGGTGGCGGC 1007
Qy 316 SerGlyGlyGlyGlySer 321
Db 1008 TCCGGTGGTGGTGGTAGC 1025

RESULT 5
US-10-491-653-25
; Sequence 25, Application US/10491653
; Publication No. US20050059082A1
; GENERAL INFORMATION:
; APPLICANT: Breitling, Frank
; APPLICANT: Moldenhauer, Gerhard
; APPLICANT: Poustka, Annemarie
; APPLICANT: Kuhlwein, Thorsten
; APPLICANT: Luttgau, Sandra
; TITLE OF INVENTION: Method for Producing Protein Libraries and for Selecting Proteins
; FILE REFERENCE: 4121-162
; CURRENT APPLICATION NUMBER: US/10/491,653
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: EP 01123596.7
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP02/10852
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 151
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 1906
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-491-653-25

Alignment Scores:
Pred. No.: 1,33e-78 Length: 1906
Score: 948.50 Matches: 186
Percent Similarity: 81.40% Conservative: 24
Best Local Similarity: 72.09% Mismatches: 39
Query Match: 54.99% Indels: 9
DB: 21 Gaps: 2

US-10-089-278-6 (1-329) x US-10-491-653-25 (1-1906)
Qy 44 ProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArgProGlyVal 63
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Db      908  CCACCGTCCCAAGATTACGTCAGCAGCTCTGGGCTGAACGTGTGAGGCCCTGGGGTC 967
Qy      64  SerVallylsleSerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTyr 83
Db      968  TCAGTGAAGATTCTCTGCAAGGGTCTGGCTACAAATTCATGATTATGCTAGCCACTGG 1027
Qy      84  VallysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGly 103
Db      1028  GTGMAACAGAGTCATGCAAGAGTCTAGAGTGGATTGGAGTATTAGTACTTATATGGT 1087
Qy      104  AspProSerTyrAnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSer 123
Db      1088  GATACTACTTATACCAAGAGTTCAAGGCAAGGCTCAAGGCCCAAGCCCAATGCTGCGCAAAATCCTCC 1147
Qy      124  AsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCys 143
Db      1148  AGCACAGCTTATATGGAATTCACAGACTTCCAGACTGACATCTGATGATTTCTGCAATATTATGT 1207
Qy      144  AlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTyrTyrGlyGlnGlyThr 163
Db      1208  GCC-----CTGTTAGGCCCTTTGCTTACTGGGCGCAAGGACC 1246
Qy      164  ThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGly 183
Db      1247  ACGGTACCGTCTCTCAGGTGAGGCGGTTACAGCGAGGTGGCTCTGGCGGTGGCGGA 1306
Qy      184  SerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAla 203
Db      1307  TCGGACATCGAGTCACTCAGTCTCCATCTCCCTGAGTGTGTGAGCAGGAGAGAAGGTC 1366
Qy      204  ThrIleSerCysArgAlaSerGluSerValAspSerTyrGly-----AspSerPheMet 221
Db      1367  ACTATGAGCTGCAAGTCCAGTCAAGTCTGTAAACAGTGGAAATCAAAATACAGACTTG 1426
Qy      222  HisTrpTyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSerAsn 241
Db      1427  GCCTGGTACCAGCAGAAACAGCGCAACGTCCTAATCTGTGATCAGCGGGCATCCACT 1486
Qy      242  LeuGluSerGlyValProAlaArgPheSerGlySerGlySerGlySerGluSerAspPheThrLeu 261
Db      1487  AGGGAATCTGGGTCTCCCTGATCGTTCACAGCGAGTGGATCTGGAACCGGATTTCACTCTT 1546
Qy      262  ThrIleAspProValGluGluAspAspAlaAlaValTyrTyrCysLeuGlnSerMetGlu 281
Db      1547  ACCATCAGCAGTGTGACGGCTGAAGACCTGGCAGTTTATTACTGTGCAATGATCATAGT 1606
Qy      282  AspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAla 299
Db      1607  TATCCGTTACGTTCCGTTGCTGCGCACCAAGCTGGAATCAACCGGGCGCGCT 1660

```

RESULT 6

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US-10-169-351-68
; Sequence 68, Application US/10169351
; Publication No. US20030157090A1
; GENERAL INFORMATION:
; APPLICANT: BENVENUTO, EUGENIO
; APPLICANT: FRANCONI, ROSELLA
; APPLICANT: DESIDERIO, ANGIOLA
; APPLICANT: TAVLADORAKI, PARASKEVI
; TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES
; TITLE OF INVENTION: WHICH INCLUDE THEM
; FILE REFERENCE: 4161-4
; CURRENT APPLICATION NUMBER: US/10/169,351
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/IT00/00554
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: IT RM99A000803
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 756
; TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-10-169-351-68

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Alignment Scores:
Pred. No.: 5,8e-79 Length: 756
Score: 947.50 Matches: 180
Percent Similarity: 82.61% Conservative: 29
Best Local Similarity: 71.15% Mismatches: 39
Query Match: 54.93% Indels: 5
DB: 16 Gaps: 2

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US-10-089-278-6 (1-329) x US-10-169-351-68 (1-756)

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Qy      48  GluValLysLeuGlnGlnSerGlyAlaGluLeuValArgProGlyValSerValIle 67
Db      1  CAGGTGCAGCTGCAGGAGTCTGGGGGAGACTTAGTCAGGCTCGAGGGTCCCTGAAACTC 60
Qy      68  SerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTyrValLysGlnSer 87
Db      61  TCCTGTGCAGCCTCTCGGATTCACCTTCAGTAGCTATGGCATGCTCTGGGTTCGCCAGACT 120
Qy      88  HisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107
Db      121  CMAGCAAGAGGCTGGAGTTGGTCGCAACCAATTAGTAATGGTGTAGCACCTTTTAT 180
Qy      108  AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
Db      181  CCAGACAGTGTGAGGGCGGATTCACCATCTCCAGAGACAATGCCAAGACACCTCTGAC 240
Qy      128  LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAsp 147
Db      241  CTGCAATGAGCAGTCTGAAGTCTGAGGACACAGCCATGATTACTGTGCAAGAAGA--- 297
Qy      148  GlyAsnTyrGlyTyrTyrTyrAla-----LeuAspTyrTrpGlyGlnGlyThr 163
Db      298  AGGAATTAACCTTATCTACCGTAGTAGAGGTACTTTGACTACTTGGGGCCAAAGGACC 357
Qy      164  ThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGly 183
Db      358  ACGGTACACGCTCTCTCAGGTGAGGCGGTTGAGGGCGAGGTGGCTCTGGCGGTGGCGGA 417
Qy      184  SerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAla 203
Db      418  TCGGACATCGAGTCACTCAGTCTCCAGCTTCTTGGCTGTCTCTAGGGCAGAGGGCC 477
Qy      204  ThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTrp 223
Db      478  ACCATATCTGCGAGGCCAGTGAAGTGTGATAGTTATGGCAATAGTTTATGCACTGG 537
Qy      224  TyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSerAsnLeuGlu 243
Db      538  TACCAGCAGAACCCAGCAGCAGCCCAACCTCTCTATCTATCGTGCATTAATCTAGAA 597
Qy      244  SerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIle 263
Db      598  TCTGGGATCCCTGCCAGGTTCAGTGGCAGTGGGTCTAGGACAGACTTACCCTTCCACTT 657
Qy      264  AspProValGluGluAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspPro 283
Db      658  AATCTGTGGAGGCTGATGATGTGCAACCTATTACTGTGCAAAAGTAATGAGGATCCG 717
Qy      284  TyrThrPheGlyGlyThrLysLeuGluIleLysArg 296
Db      718  TGGACGTTCCGTTGGAGGCCACCAAGCTCGAGATCAAAACGG 756

```

RESULT 7

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US-09-808-037-5
; Sequence 5, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:

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Qy 148 GlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrThrValThrVal 167
Db 298 GCTACTATGCTCTACTTT-----GACTACTGGGGCCCAAGTGACCAAGGTACCGGTC 348
Qy 168 SerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGlySerAspIleGlu 187
Db 349 TCCTCAGGTGAGCGCGGTTCAGGCGGAGTTGGCTCTGGCGGTGGCGGATCGGACATCGAG 408
Qy 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
Db 409 CTCACTCAGTCTCAGCAATCATGCTGCATCTCCAGGGGGAAGGTCCACATGACCTGC 468
Qy 208 ArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTyrTrpGlnGlnLys 227
Db 469 AGTCCAGCTCAAGTATA-----AGTTACATGCACTGGTATCAGCAGAG 513
Qy 228 ProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGlyValPro 247
Db 514 CCAGGCACCTCCCCCAAAAGATGATTTATGACACATCCAAACTCGGCTTCTGGAGTCCCT 573
Qy 248 AlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspProValGlu 267
Db 574 GCTCGCTCAGTGGCAGTGGGTCTGGGACCTCTTATTCTCTCAAAATCAGCAGATGGAG 633
Qy 268 GluAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGly 287
Db 634 GCTGAAGATGCTGCCACTTATTACTGCATCAGCGGAGTAGTTACCACTTACGCTTCGGA 693
Qy 288 GlyGlyThrLysLeuGluIleLys 295
Db 694 GGGGGGGCCCAAGCTGGAAATAAAA 717

RESULT 9

US-10-384-788-5
; Sequence 5, Application US/10384788
; Publication No. US20040013647A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: FRENKEL, Dan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A PLAQUE-FORMING DISEASE
; FILE REFERENCE: SOLOMON-2D.2
; CURRENT APPLICATION NUMBER: US/10/384,788
; CURRENT FILING DATE: 2003-03-11

; PRIOR APPLICATION NUMBER: 60/371,735
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 09/808,037
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/830,954
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 10/162,889
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/152,417
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/IL00/00518
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 717

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-384-788-5

Alignment Scores: 7.19e-78 Length: 717
Pred. No.: 935.50 Matches: 181
Score:

Percent Similarity: 81.85% Conservative: 22
Best Local Similarity: 72.98% Mismatches: 36
Query Match: 54.23% Indels: 9
DB: 17 Gaps: 3

US-10-089-278-6 (1-329) x US-10-384-788-5 (1-717)

Qy 48 GluValLysLeuGlnSerGlyAlaGluLeuValArgProGlyValSerValLysIle 67
Db 1 CAGGTCAAACTGCAGGAGTCAGGGGCTGAGCTGGTGAGGCTGGGGTCTCAGTGAAGATT 60
Qy 68 SerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpValLysGlnSer 87
Db 61 TCCTGCAAGGTTCTGGCTACACATTCACATGATTATGCTATGCACTGGTCAAGCAGAGT 120
Qy 88 HisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107
Db 121 CATGCCAAAGATCTCAGAGTGGATTGGAGTTATTAGTACTTACTATGTTGATGCTAGCTAC 180
Qy 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerAsnThrAlaTyr 127
Db 181 AACCAAGATTCAAGGGCAAGGCCAATGACTGTAGACAAATCCTCCAGCAGCCTAT 240
Qy 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAsp 147
Db 241 ATGGAATTCGCAGACTGACATCTGAGGATCTGCCATCTATTACTGTGCAAGAGGG--- 297
Qy 148 GlyAsnTyrGlyTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrThrValThrVal 167
Db 298 GCTACTATGCTCTACTTT-----GACTACTGGGGCCCAAGTGACACGGTCACCGTC 348
Qy 168 SerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGlySerAspIleGlu 187
Db 349 TCCTCAGGTGAGCGGTTTCAGGCGGAGTTGGGCTCTGGCGGTGGCGGATCGGACATCGAG 408
Qy 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
Db 409 CTCACTCAGTCTCAGCAATCATGCTGCATCTCCAGGGGGAAGGTCCACATGACCTGC 468
Qy 208 ArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTyrTrpGlnGlnLys 227
Db 469 AGTCCAGCTCAAGTATA-----AGTTACATGCACTGGTATCAGCAGAG 513
Qy 228 ProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGlyValPro 247
Db 514 CCAGGCACCTCCCCCAAAAGATGATTTATGACACATCCAAACTGGGCTTCTGGAGTCCCT 573
Qy 248 AlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspProValGlu 267
Db 574 GCTCGCTCAGTGGCAGTGGGTCTGGGACCTCTTATTCTCTCAAAATCAGCAGATGGAG 633
Qy 268 GluAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGly 287
Db 634 GCTGAAGATGCTGCCACTTATTACTGCATCAGCGGAGTAGTTACCACTTACGCTTCGGA 693
Qy 288 GlyGlyThrLysLeuGluIleLys 295
Db 694 GGGGGGGCCCAAGCTGGAAATAAAA 717

RESULT 10

US-10-618-856-5
; Sequence 5, Application US/10618856
; Publication No. US20040052766A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: FRENKEL, Dan
; TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY
; FILE REFERENCE: SOLOMON-2A
; CURRENT APPLICATION NUMBER: US/10/618,856
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/473,653A
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417

;
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-618-856-5

Alignment Scores:
Pred. No.: 7,19e-78 Length: 717
Score: 935.50 Matches: 181
Percent Similarity: 81.85% Conservative: 22
Best Local Similarity: 72.98% Mismatches: 36
Query Match: 54.23% Indels: 9
DB: 18 Gaps: 3

US-10-089-278-6 (1-329) x US-10-618-856-5 (1-717)

```
QY 48 GluValLysLeuGlnSerGlyAlaGluLeuValArgProGlyValSerValLysIle 67
   :::::::::::::::::::::
Db 1 CAGGTCAAACTGCAGGAGTCAGGGGCTGAGCTGGTGAGGCTCTCAGTGAAGATT 60

QY 68 SerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpValLysGlnSer 87
   :::::::::::::::::::::
Db 61 TCCTGCAAGGTTCTGGCTACACATTTCACGTGATTGCTATGCATGGGTGAAGCAGATT 120

QY 88 HisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107
   :::::::::::::::::::::
Db 121 CATGCAAAAGAGTCTAGAGTGGATTGGAGTTATTAGTACTTACTATGGTGTAGCTACTAC 180

QY 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
   :::::::::::::::::::::
Db 181 AACCCAGAGTTCAAGGGCAAGGCCAATGACTGTAGACAAATCCTCCAGCACAGCCTAT 240

QY 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAsp 147
   :::::::::::::::::::::
Db 241 ATGGAACTTCCAGACTGACATCTGAGGATCTGCCATCTATTACTGTGCAAGAGG--- 297

QY 148 GlyAsnTyrGlyTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrThrValThrVal 167
   :::::::::::::::::::::
Db 298 GCTACTATGCTCTACTTT-----GACTACTGGGGCCAGTGCACCGTCCACGTC 348

QY 168 SerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGlyGlyGlyGlyGlu 187
   :::::::::::::::::::::
Db 349 TCCTCAGGTGGAGCGGTTCCAGCGGAGTTGGCTCTGGCGGTGGCGATCGGAATCGAG 408

QY 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
   :::::::::::::::::::::
Db 409 CTCACCTCAGTCTCCAGCAATCATGCTCGCATCTCCAGGGGAGGAAGGTCCACCATGACCTGC 468

QY 208 ArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTrpTyrGlnGlnLys 227
   :::::::::::::::::::::
Db 469 AGTGCACGCTCAAGTATA-----AGTTACATGCATCGCTATCAGCAGAAG 513

QY 228 ProGlyClnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGlyValPro 247
   :::::::::::::::::::::
Db 514 CCAGGCACCTCCCCCAAAAGATGGATTATGACACATCCAAACTGGCTCTCGGAGTCCCT 573

QY 248 AlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspProValGlu 267
   :::::::::::::::::::::
Db 574 GCTCGCTTCACTGGCAGTGGGTCTGGACCTCTATTCTCTCAATCAGCACATGGAG 633

QY 268 GluAspAspAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGly 287
   :::::::::::::::::::::
Db 634 GCTGAAGATGCTGCCACTTATTACTGCGCATCAGCGGAGTAGTTACCCATTACGTTCCGA 693

QY 288 GlyGlyThrLysLeuGluIleLys 295
   :::::::::::::::::::::
Db 694 GGGGGGGCCAAAGCTGGAAATAAAA 717
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RESULT 11

US-10-749-522-5
; Sequence 5, Application US/10749522
; Publication No. US20050089510A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beki
; APPLICANT: HANAN, Elia
; TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN DIAG
; TITLE OF INVENTION: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
; FILE REFERENCE: SOLOMON=2B
; CURRENT APPLICATION NUMBER: US/10/749,522
; CURRENT FILING DATE: 2004-01-02
; PRIOR APPLICATION NUMBER: US/09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-749-522-5

Alignment Scores:
Pred. No.: 7,19e-78 Length: 717
Score: 935.50 Matches: 181
Percent Similarity: 81.85% Conservative: 22
Best Local Similarity: 72.98% Mismatches: 36
Query Match: 54.23% Indels: 9
DB: 21 Gaps: 3

US-10-089-278-6 (1-329) x US-10-749-522-5 (1-717)

```
QY 48 GluValLysLeuGlnSerGlyAlaGluLeuValArgProGlyValSerValLysIle 67
   :::::::::::::::::::::
Db 1 CAGGTCAAACTGCAGGAGTCAGGGGCTGAGCTGGTGAGGCTCTCAGTGAAGATT 60

QY 68 SerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpValLysGlnSer 87
   :::::::::::::::::::::
Db 61 TCCTGCAAGGTTCTGGCTACACATTTCACGTGATTGCTATGCATGGGTGAAGCAGATT 120

QY 88 HisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107
   :::::::::::::::::::::
Db 121 CATGCAAAAGAGTCTAGAGTGGATTGGAGTTATTAGTACTTACTATGGTGTAGCTACTAC 180

QY 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
   :::::::::::::::::::::
Db 181 AACCCAGAGTTCAAGGGCAAGGCCAATGACTGTAGACAAATCCTCCAGCACAGCCTAT 240

QY 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAsp 147
   :::::::::::::::::::::
Db 241 ATGGAACTTCCAGACTGACATCTGAGGATCTGCCATCTATTACTGTGCAAGAGG--- 297

QY 148 GlyAsnTyrGlyTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrThrValThrVal 167
   :::::::::::::::::::::
Db 298 GCTACTATGCTCTACTTT-----GACTACTGGGGCCAGTGCACCGTCCACGTC 348

QY 168 SerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGlyGlyGlyGlyGlu 187
   :::::::::::::::::::::
Db 349 TCCTCAGGTGGAGCGGTTCCAGCGGAGTTGGCTCTGGCGGTGGCGATCGGAATCGAG 408

QY 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
   :::::::::::::::::::::
Db 409 CTCACCTCAGTCTCCAGCAATCATGCTCGCATCTCCAGGGGAGGAAGGTCCACCATGACCTGC 468

QY 208 ArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTrpTyrGlnGlnLys 227
   :::::::::::::::::::::
Db 469 AGTGCACGCTCAAGTATA-----AGTTACATGCATCGCTATCAGCAGAAG 513
```


Query Match: 54.20% Indels: 36
DB: 9 Gaps: 4

US-10-089-278-6 (1-329) x US-09-742-693-27 (1-996)

QY 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnGlnSerGlyAlaGluLeuValArg 60
DB 85 GCTGCCAACCGCCATGGCCAGGTGCGAGTCGACGAGTCTGGGCTGAACCTGGTGAAG 144
QY 61 ProGlyValSerValLysLysSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
DB 145 CTTGGGCCCTTCTGTGAAGTGTCTCTCAAGGCTTCGAGCTACACCTTCACCACTATTGG 204
QY 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuLysSerThr 100
DB 205 ATGCACCTGGGTGAAGCAGAGCCCTGCACAGGCTTGAGTGGATTGGAGATTATCT 264
QY 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
DB 265 ACCAACGGTCTGATTATTACATGAGAGTTCAAGAGCAAGCCACACTGACTGTAGAC 324
QY 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
DB 325 AAATCTCCAGTACAGCCTACATCGAGCTCGAGCTGACATCTGAGGACTCTGCGGTC 384
QY 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrAlaLeuAspTyrTrpGly 160
DB 385 TATTACTGTGCAAGAGGTATGTTAC-----TCCTTTGACTCTGGGC 429
QY 161 GlnGlyThrThrValThrValSerSer----- 169
DB 430 CAAGGACCAACGCTCACCGTCTCTCATATAAGAGCTATGGGAGCTTGCATCAAAATC 489
QY 170 -----GlyGlyGlyGlySerGly 175
DB 490 TATTTCAAGGAGACAGTCATAATGAATACCTATTGCCTACGCGACCGCTGGATTGTTA 549
QY 176 GlyGlyGlySerGlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeu 195
DB 550 TTACTCGTCCCAACACGAGGTGGCGACATCGAGCTACCCAGTCTCCAGATTTCTTG 609
QY 196 AlaValSerLeuGlyGlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSer 215
DB 610 GCTGTGTCTCTAGGGCAGAGGGCCACCATATCTCGCAGAGCCAGTGAAAGTGTGATAGT 669
QY 216 TyrGlyAspSerPheMetHisTrpTyrGlnGlnLysProGlyGlnProProLysLeuLeu 235
DB 670 TATGGCAATAGTTTTATGCAAGTGGTACCAGCAGAAACCCAGGACGCCCAAACTCCCTC 729
QY 236 IleTyrArgAlaSerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySer 255
DB 730 ATCTATCGTCATCCAACTAGAAATCTGGATTCTGGCAGGTTCTAGTGGCAGTGGGTCT 789
QY 256 GluSerAspPheThrLeuThrIleAspProValGluGluAspAlaAlaValTyrTyr 275
DB 790 AGGACAGACTTCACCTCACCATTATCTCTGAGGCTGATGATGTTGCAACCTATTAT 849
QY 276 CysLeuGlnSerMetGluAspPro-----TyrThrPheGlyGlyThrLysLeuGlu 293
DB 850 TGTCAACAAAGTATGATGATTCGATACATGATACGTTGCGAGGGGGGACCAAGCTCGAG 909
QY 294 IleLysArgAlaAlaAlaSerGlySerGlyGlyGlySerGlyGlyGly 310
DB 910 ATCAACGG-----GGATCGGTAGCGGGNACTCCGGTAAAGGG 948

RESULT 14

US-10-089-994-13
; Sequence 13, Application US/10879994
; Publication No. US20050032175A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Yancopoulos, George D.
; APPLICANT: Karow, Margaret

; APPLICANT: Smith, Eric
; TITLE OF INVENTION: HIGH AFFINITY FUSION PROTEINS AND THERAPEUTIC AND DIAGNOSTIC METH
; FILE REFERENCE: REG 203E2
; CURRENT APPLICATION NUMBER: US/10/879,994
; CURRENT FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: 10/610,452
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 744
; TYPE: DNA
; ORGANISM: mus musculus
US-10-879-994-13

Alignment Scores:
Pred. No.: 1.43e-77 Length: 744
Score: 932.50 Matches: 180
Percent Similarity: 82.40% Conservative: 26
Best Local Similarity: 72.00% Mismatches: 41
Query Match: 54.06% Indels: 3
DB: 21 Gaps: 2

US-10-089-278-6 (1-329) x US-10-879-994-13 (1-744)

QY 48 GluValLysLeuGlnGlnSerGlyAlaGluLeuValArgProGlyValSerValLysIle 67
DB 1 CAGGTCACGCTTCAGCAGTCTGGGCTGAACTGGCAAAACCTGGGCGCTCAGTGAAGATG 60
QY 68 SerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpValLysGlnSer 87
DB 61 TCTCGAAGGCTTCGGCTAGACCTTTACTAGTACTGCGATGCGACTGATAAAACAGAGG 120
QY 88 HisAlaLysSerLeuGluTrpIleGlyLeuLysSerThrTyrTyrGlyAspProSerTyr 107
DB 121 CTTGGACAGGCTCTGGATGGATTGGATACATTAATCTTAGCAGCTGTTATCTAGTATC 180
QY 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
DB 181 AATCAAGATTTCAAGCAAGGCCCATTTGACTGCGAGCAAAATCTTCCAGCAGCGCTAC 240
QY 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAsp 147
DB 241 ATGCAACTCAGCAGCGCTGACATCTGAGGACTCTGCACTCTATTACTGTGCAAGGGAC--- 297
QY 148 GlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrThrValThrVal 167
DB 298 ---TACTATGATTACGAAGATGTTATGGACTACTGGGGTCAAGGAACCTCAGTCAACGTC 354
QY 168 SerSer---GlyGlyGlySerGlyGlyGlySerGlyGlySerGlyGlySerAspIle 186
DB 355 TCTTCAGCGGTGGAGCGGTTCAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATT 414
QY 187 GluLeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSer 206
DB 415 GTGCTCACCAATCTCCAGCTCTTTGGCTGTGTCTTAGGGCAGAGGGCCACCACTCC 474
QY 207 CysArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTrpTyrGlnGln 226
DB 475 TGCAGAGCCAGCGAAAGTGTGATGGTTTGGCATTTAGTTTATGAACCTGGTTCCAAACAG 534
QY 227 LysProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGlyVal 246
DB 535 AAACACAGGACAGCCCAACCTCTCATCTATCTGCTGCATCCCAACAGGATCCGGGGTC 594
QY 247 ProAlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspProVal 266
DB 595 CTTGCCAGGTTTAGTGGCAGTGGTCTGGGACAGACTTCCAGCCTCAACATCCATCTATG 654
QY 267 GluLysAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPhe 286
DB 655 GAGGAGGGTGTGCTGCAATGTATTTCTGTGCAGCAAAATTAAGGAGGTTCCGTGGACGTTT 714

QY 287 GlyGlyGlyThrLeuLeuGluLeuLeuValArg 296
|||||
Db 715 GGTGGAGGCCCAAGCTGGAAATCAAAACGG 744

RESULT 15

US-10-610-452-13
; Sequence 13, Application US/10610452
; Publication No. US20050074855A1
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl
; APPLICATOR: George D. Yancopoulos
; TITLE OF INVENTION: Cytokine-Specific Fusion Proteins and
; TITLE OF INVENTION: Therapeutic and Diagnostic Methods for Use
; FILE REFERENCE: REG 203E
; CURRENT APPLICATION NUMBER: US/10/610,452
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: PCT/US9/22045
; PRIOR FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1999-09-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 744
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-610-452-13

Alignment Scores:

Pred. No.:	1.43e-77	Length:	744
Score:	932.50	Matches:	180
Percent Similarity:	82.40%	Conservative:	26
Best Local Similarity:	72.00%	Mismatches:	41
Query Match:	54.06%	Indels:	3
DB:	21	Gaps:	2

US-10-089-278-6 (1-329) x US-10-610-452-13 (1-744)

QY 48 GluValLeuGlnGlnSerGlyAlaGluLeuValArgProGlyValSerValLysIle 67
:::|||||
Db 1 CAGGTCAGGCTTCAGGAGCTGGGGCTGAACCTGGCAAACTGGGGCTCAGTGAAGATG 60
68 SerCysLysGlySerGlyThrPheThrAspTyrGlyMetSerTrpValLysGlnSer 87
61 TCCTGCAGGCTTCGGCTACACCTTTACTAGCTACCTAGCTGGATGCACTGGATAAACAGAGG 120
QY 88 HisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107
:::|||||
Db 121 CTGGACAGGGCTCGGAATGGATTGGATACATTAACTAGCTAGCTGGATGCACTGGATTAACAGAGTAC 180
QY 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
|||||
Db 181 AATCAGAAGTTCAAGGACCAAGGCCACATTGACTGCACAGCAAAATCTCCAGCACAGCCTAC 240
QY 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAsp 147
:::|||||
Db 241 ATGCAACTGAGAGCTTGACATCTGAGGACTCTGCAGCTCTATTACTGTGCAAGGGAC--- 297
QY 148 GlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrValThrVal 167
|||||
Db 298 ---TACTATGATTACCAAGATGTTATGGACTACTGGGGTCAAGGAACCTCAGTCAACGTC 354
QY 168 SerSer---GlyGlyGlySerGlyGlyGlySerGlyGlySerGlyGlySerAspIle 186
|||||
Db 355 TCCTCAGCGGTGGAGCGGCTTCAGGCGAGGTGGCTCTGGCGGTGGCGGATCGGACATT 414
QY 187 GluLeuThrGlnSerProSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSer 206
|||||

Db 415 GTGCTGACCCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTCC 474
QY 207 CysArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTrpTyrGlnGln 226
|||||
Db 475 TGCAGAGCCAGCGAAAGTGTGATGGTTTGGCAITAGTTTATGAACCTGGTTCCACAG 534
QY 227 LysProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGlyVal 246
|||||
Db 535 AAACAGGACAGCCACCCAACTCTCTCATCTATGCTGCATCCAAACCAAGGATCGGGGTC 594
QY 247 ProAlaArgPheSerGlySerGluSerGlySerPheThrLeuThrIleAspProVal 266
|||||
Db 595 CCTGCCAGGTTTAGTGGCAGTGGTCTGGGACAGACTTCAGCCTCAACATCCATCTATG 654
QY 267 GluGluAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPhe 286
|||||
Db 655 GAGGAGGCTGATGCTGCAATGATTTCTGTCAGCAAAATTAAGGAGGTTCGTTGGACGTTT 714
QY 287 GlyGlyGlyThrLysLeuGluIleLysArg 296
Db 715 GGTGGAGGCCCAAGCTGGAAATCAAAACGG 744

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